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(54) Title: SOLUBLE PEPTIDES HAVING CONSTRAINED, SECONDARY CONFORMATION IN SOLUTION AND METHOD OF MAKING SAME (57) Abstract A method of synthesizing isolated, soluble peptides having constrained secondary structure in solution is described herein. The peptides are encoded by expressible oligonucleotides having a desirable bias of random codon sequences.		

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SOLUBLE PEPTIDES HAVING
CONSTRAINED, SECONDARY CONFORMATION IN
SOLUTION AND METHOD OF MAKING SAME

BACKGROUND OF THE INVENTION

5 The biological function of a peptide depends upon its direct, physical interaction with another molecule. The peptide or protein is termed the ligand.

 Peptides are distinguishable by their specificity for certain ligand-binding proteins. The specificity of
10 binding, i.e., the discrimination between closely related ligands, is determined by a peptide's binding affinity. Peptides having useful binding properties are invaluable for chemotherapy and drug design. Therefore, a need exists for the generation of peptides having biologically useful
15 binding affinities and being soluble in solution.

 Secondary structure of a peptide is critical for determining its binding affinity. For example, a highly flexible peptide is able to interact with many distinct molecules; however, the peptide-ligand interaction is
20 easily disrupted, or in other words, the binding affinity of the peptide is low. Thus, a peptide having a specific secondary structure is able to bind tightly with only a few or one ligand.

 However, if secondary structure of the ligand
25 results from non-covalent interactions, the peptide inevitably is insoluble. Intra-peptide covalent bonds can solve this problem resulting in constrained peptides, i.e., peptides having a stable secondary structure in a solution, that are soluble.

30 This invention provides a method to synthesize soluble peptides having constrained, secondary conformation in solution, as well as the peptides produced by this method.

This invention also relates generally to methods for synthesizing and expressing oligonucleotides and, more particularly, to methods for expressing oligonucleotides having biased, but random codon sequences.

5 Oligonucleotide synthesis proceeds via linear coupling of individual monomers in a stepwise reaction. The reactions are generally performed on a solid phase support by first coupling the 3' end of the first monomer to the support. The second monomer is added to the 5' end
10 of the first monomer in a condensation reaction to yield a dinucleotide coupled to the solid support. At the end of each coupling reaction, the by-products and unreacted, free monomers are washed away so that the starting material for the next round of synthesis is the pure oligonucleotide
15 attached to the support. In this reaction scheme, the stepwise addition of individual monomers to a single, growing end of a oligonucleotide ensures accurate synthesis of the desired sequence. Moreover, unwanted side reactions are eliminated, such as the condensation of two
20 oligonucleotides, resulting in high product yields.

 In some instances, it is desired that synthetic oligonucleotides have random nucleotide sequences. This result can be accomplished by adding equal proportions of all four nucleotides in the monomer coupling reactions,
25 leading to the random incorporation of all nucleotides and yielding a population of oligonucleotides with random sequences. Since all possible combinations of nucleotide sequences are represented within the population, all possible codon triplets will also be represented. If the
30 objective is ultimately to generate random peptide products, this approach has a severe limitation because the random codons synthesized will bias the amino acids incorporated during translation of the DNA by the cell into polypeptides.

The bias is due to the redundancy of the genetic code. There are four nucleotide monomers which leads to sixty-four possible triplet codons. With only twenty amino acids to specify, many of the amino acids are encoded by multiple codons. Therefore, a population of oligonucleotides synthesized by sequential addition of monomers from a random population will not encode peptides whose amino acid sequence represents all possible combinations of the twenty different amino acids in equal proportions. That is, the frequency of amino acids incorporated into polypeptides will be biased toward those amino acids which are specified by multiple codons.

To alleviate amino acid bias due to the redundancy of the genetic code, the oligonucleotides can be synthesized from nucleotide triplets. Here, a triplet coding for each of the twenty amino acids is synthesized from individual monomers. Once synthesized, the triplets are used in the coupling reactions instead of individual monomers. By mixing equal proportions of the triplets, synthesis of oligonucleotides with random codons can be accomplished. However, this is not possible because of the inefficiency of the coupling, which is less than 3% and the high cost of synthesis.

Amino acid bias can be reduced, however, by synthesizing the degenerate codon sequence NNK where N is a mixture of all four nucleotides and K is a mixture of guanine and thymine nucleotides. Each position within an oligonucleotide having this codon sequence will contain a total of 32 codons (12 encoding amino acids being represented once, 5 represented twice, 3 represented three times and one codon being a stop codon). Oligonucleotides expressed with such degenerate codon sequences will produce peptide products whose sequences are biased toward those amino acids being represented more than once. Thus, populations of peptides whose sequences are completely

random cannot be obtained from oligonucleotides synthesized from d generate sequences.

There thus exists a need for a method to express oligonucleotides having a fully random or desirably biased
5 sequence which alleviates genetic redundancy. The present invention satisfies these needs and provides additional advantages as well.

SUMMARY OF THE INVENTION

This invention provides a peptide having
10 constrained, secondary structure in solution as well as methods of synthesizing these peptides.

The invention provides a plurality of procaryotic cells containing a diverse population of expressibl oligonucleotides encoding soluble peptides having
15 constrained secondary structure or conformation in solution, the expressible oligonucleotide being operationally linked to expression elements, the expressible oligonucleotides further characterized as having a desirable bias of random codon sequences.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a schematic drawing for synthesizing oligonucleotides from nucleotide monomers with random
20 tuplets at each position using twenty reaction vessels.

Figure 2 is a schematic drawing for synthesizing
25 oligonucleotides from nucleotide monomers with random tuplets at each position using ten reaction vessels.

Figure 3 is a schematic diagram of the two vectors used for sublibrary and library production from precursor oligonucleotide portions. Mi3IX22 (Figure 3A) is

the vector used to clone the anti-sense precursor portions (hatched box). The single-headed arrow r presents the Lac p/o expression sequences and the double-headed arrow represents the portion of M13IX22 which is to be combined with M13IX42. The amber stop codon for biological selection and relevant restriction sites are also shown. M13IX42 (Figure 3B) is the vector used to clone the sense precursor portions (open box). Thick lines represent the pseudo-wild type (ϕ gVIII) and wild type (gVIII) gene VIII sequences. The double-headed arrow represents the portion of M13IX42 which is to be combined with M13IX22. The two amber stop codons and relevant restriction sites are also shown. Figure 3C shows the joining of vector population from sublibraries to form the functional surface expression vector M13IX. Figure 3D shows the generation of a surface expression library in a non-suppressor strain and the production of phage. The phage are used to infect a suppressor strain (Figure 3E) for surface expression and screening of the library.

Figure 4 is a schematic diagram of the vector used for generation of surface expression libraries from random oligonucleotide populations (M13IX30). The symbols are as described for Figure 3.

Figure 5 is the nucleotide sequence of M13IX42 (SEQ ID NO: 1).

Figure 6 is the nucleotide sequence of M13IX22 (SEQ ID NO: 2).

Figure 7 is the nucleotide sequence of M13IX30 (SEQ ID NO: 3).

Figure 8 is the nucleotide sequence of M13ED03 (SEQ ID NO: 4).

Figure 9 is the nucleotide sequence of M13IX421 (SEQ ID NO: 5).

Figure 10 is the nucleotide sequence of M13ED04 (SEQ ID NO: 6).

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DETAILED DESCRIPTION OF THE INVENTION

This invention is directed to a simple and inexpensive method for synthesizing and expressing oligonucleotides having a desirable bias of random codons using individual monomers. The oligonucleotides produced
10 by this method encode soluble peptides having constrained secondary structure in solution. The method is advantageous in that individual monomers are used instead of triplets and by synthesizing only a non-degenerate subset of all triplets, codon redundancy is alleviated.
15 Thus, the oligonucleotides synthesized represent a large proportion of possible random triplet sequences which can be obtained. The oligonucleotides can be expressed, for example, on the surface of filamentous bacteriophage in a form which does not alter phage viability or impose
20 biological selections against certain peptide sequences. The oligonucleotides produced are therefore useful for generating an unlimited number of pharmacological and research products.

This invention entails the sequential coupling of
25 monomers to produce oligonucleotides with a desirable bias of random codons. The coupling reactions for the randomization of twenty codons which specify the amino acids of the genetic code are performed in ten different reaction vessels. Each reaction vessel contains a support
30 on which the monomers for two different codons are coupled in three sequential reactions. One of the reactions couples an equal mixture of two monomers such that the final product has two different codon sequences. The

codons are randomized by removing the supports from the reaction vessels and mixing them to produce a single batch of supports containing all twenty codons at a particular position. Synthesis at the next codon position proceeds by
5 equally dividing the mixed batch of supports into ten reaction vessels as before and sequentially coupling the monomers for each pair of codons. The supports are again mixed to randomize the codons at the position just synthesized. The cycle of coupling, mixing and dividing
10 continues until the desired number of codon positions have been randomized. After the last position has been randomized, the oligonucleotides with random codons are cleaved from the support. The random oligonucleotides can then be expressed, for example, on the surface of
15 filamentous bacteriophage as gene VIII-peptide fusion proteins. Alternative genes can be used as well. Using this method, one can randomize oligonucleotides at certain positions and select for specific oligonucleotides at others.

20 This invention provides a diverse population of synthetic biased oligonucleotides contained in vectors so as to be expressible in cells. In the preferred embodiment of this invention, the oligonucleotides are fully defined in that at least two codons encode amino acids capable of
25 forming a covalent bond. The populations of oligonucleotides can be expressed as fusion products in combination with surface proteins of filamentous bacteriophage, such as M13, as with gene VIII. The vectors can be transfected into a plurality of cells, such as the
30 procaryote E. coli.

In one embodiment, the diverse population of oligonucleotides can be formed by randomly combining first and second precursor populations, each or either precursor population having a desirable bias of random codon
35 sequences. Methods of synthesizing and expressing the

diverse population of expressible oligonucleotides are also provided.

Two precursor populations of random precursor oligonucleotides are synthesized in one embodiment. The oligonucleotides within each population encode a portion of the final oligonucleotide that is expressed. Oligonucleotides within one precursor population encode the carboxy terminal portion of the expressed oligonucleotides. In one embodiment, these oligonucleotides are cloned in frame with a gene VIII (gVIII) sequence so that translation of the sequence produces peptide fusion proteins. The second population of precursor oligonucleotides are cloned into a separate vector. Each precursor oligonucleotide within this population encodes the anti-sense of the amino terminal portion of the expressed oligonucleotides. This vector also contains the elements necessary for expression. The two vectors containing the random oligonucleotides are combined such that the two precursor oligonucleotide portions are joined together at random to form a population of larger oligonucleotides derived from two smaller portions. The vectors contain selectable markers to ensure maximum efficiency in joining together the two oligonucleotide populations. A mechanism also exists to control the expression of gVIII-peptide fusion proteins during library construction and screening.

As used herein, the term "monomer" or "nucleotide monomer" refers to individual nucleotides used in the chemical synthesis of oligonucleotides. Monomers that can be used include both the ribo- and deoxyribo- forms of each of the five standard nucleotides (derived from the bases adenine (A or dA, respectively), guanine (G or dG), cytosine (C or dC), thymine (T) and uracil (U)). Derivatives and precursors of bases such as inosine which are capable of supporting polypeptide biosynthesis are also included as monomers. Also included are chemically

modified nucleotides, for example, one having a reversible blocking agent attached to any of the positions on the purine or pyrimidine bases, the ribose or deoxyribose sugar or the phosphate or hydroxyl moieties of the monomer. Such blocking groups include, for example, dimethoxytrityl, benzoyl, isobutyryl, beta-cyanoethyl and diisopropylamine groups, and are used to protect hydroxyls, exocyclic amines and phosphate moieties. Other blocking agents can also be used and are known to one skilled in the art.

10 As used herein, the term "tuplet" refers to a group of elements of a definable size. The elements of a tuplet as used herein are nucleotide monomers. For example, a tuplet can be a dinucleotide, a trinucleotide or can also be four or more nucleotides.

15 As used herein, the term "codon" or "triplet" refers to a tuplet consisting of three adjacent nucleotide monomers which specify one of the twenty naturally occurring amino acids found in polypeptide biosynthesis. The term also includes nonsense, or stop, codons which do not specify any amino acid.

25 "Random codons" or "randomized codons," as used herein, refers to more than one codon at a position within a collection of oligonucleotides. The number of different codons can be from two to twenty at any particular position. "Randomized oligonucleotides," as used herein, refers to a collection of oligonucleotides with random codons at one or more positions. "Random codon sequences" as used herein means that more than one codon position within a randomized oligonucleotide contains random codons. For example, if randomized oligonucleotides are six nucleotides in length (i.e., two codons) and both the first and second codon positions are randomized to encode all twenty amino acids, then a population of oligonucleotides having random codon sequences with every possible

combination of the twenty triplets in the first and second position makes up the above population of randomized oligonucleotides. The number of possible codon combinations is 20^3 . Likewise, if randomized
5 oligonucleotides of fifteen nucleotides in length are synthesized which have random codon sequences at all positions encoding all twenty amino acids, then all triplets coding for each of the twenty amino acids will be found in equal proportions at every position. The
10 population constituting the randomized oligonucleotides will contain 20^{15} different possible species of oligonucleotides. "Random tuplets," or "randomized tuplets" are defined analogously.

As used herein, the term "bias" refers to a
15 preference. It is understood that there can be degrees of preference or bias toward codon sequences which encode particular amino acids. For example, an oligonucleotide whose codon sequences do not preferably encode particular amino acids is unbiased and therefore completely random.
20 The oligonucleotide codon sequences can also be biased toward predetermined codon sequences or codon frequencies and while still diverse and random, will exhibit codon sequences biased toward a defined, or preferred, sequence. "A desirable bias of random codon sequences" as used
25 herein, refers to the predetermined degree of bias which can be selected from totally random to essentially, but not totally, defined (or preferred). There must be at least one codon position which is variable, however.

As used herein, the term "support" refers to a
30 solid phase material for attaching monomers for chemical synthesis. Such support is usually composed of materials such as beads of control pore glass but can be other materials known to one skilled in the art. The term is also meant to include one or more monomers coupled to the
35 support for additional oligonucleotide synthesis reactions.

As used herein, the terms "coupling" or "condensing" refers to the chemical reactions for attaching one monomer to a second monomer or to a solid support. Such reactions are known to one skilled in the art and are typically performed on an automated DNA synthesizer such as a MilliGen/Biosearch Cyclone Plus Synthesizer using procedures recommended by the manufacturer. "Sequentially coupling" as used herein, refers to the stepwise addition of monomers.

10 The term "soluble peptide" means a peptide that is soluble at a concentration equivalent to its affinity to a receptor. The peptide can then be used in aqueous solution without being attached to a cell or phage.

The term "constrained secondary structure in solution" means a peptide having a covalent bond that is not the backbone peptide bond.

A method of synthesizing oligonucleotides having biased random tuplets using individual monomers is described. The method consists of several steps, the first being synthesis of a nucleotide tuplet for each tuplet to be randomized. As described here and below, a nucleotide triplet (i.e., a codon) will be used as a specific example of a tuplet. Any size tuplet will work using the methods disclosed herein, and one skilled in the art would know how to use the methods to randomize tuplets of any size.

If the randomization of codons specifying all twenty amino acids is desired at a position, then twenty different codons are synthesized. Likewise, if randomization of only ten codons at a particular position is desired then those ten codons are synthesized. Randomization of codons from two to sixty-four can be accomplished by synthesizing each desired triplet. Preferably, randomization of from two to twenty codons is

used for any one position because of the redundancy of the genetic code. The codons selected at one position do not have to be the same codons selected at the next position. Additionally, the sense or anti-sense sequence
5 oligonucleotide can be synthesized. The process therefore provides for randomization of any desired codon position with any number of codons. In addition, it also allows one to preselect a specified codon to be present at a particular position within a randomized sequence.

10 Codons to be randomized are synthesized sequentially by coupling the first monomer of each codon to separate supports. The supports for the synthesis of each codon can, for example, be contained in different reaction vessels such that one reaction vessel corresponds to the
15 monomer coupling reactions for one codon. As will be used here and below, if twenty codons are to be randomized, then twenty reaction vessels can be used in independent coupling reactions for the first twenty monomers of each codon. Synthesis proceeds by sequentially coupling the second
20 monomer of each codon to the first monomer to produce a dimer, followed by coupling the third monomer for each codon to each of the above-synthesized dimers to produce a trimer (Figure 1, step 1, where M_1 , M_2 and M_3 represent the first, second and third monomer, respectively, for each
25 codon to be randomized).

Following synthesis of the first codons from individual monomers, the randomization is achieved by mixing the supports from all twenty reaction vessels which contain the individual codons to be randomized. The solid
30 phase support can be removed from its vessel and mixed to achieve a random distribution of all codon species within the population (Figure 1, step 2). The mixed population of supports, constituting all codon species, are then redistributed into twenty independent reaction vessels
35 (Figure 1, step 3). The resultant vessels are all

identical and contain equal portions of all twenty codons coupled to a solid phase support.

For randomization of the second position codon, synthesis of twenty additional codons is performed in each of the twenty reaction vessels produced in step 3 as the condensing substrates of step 1 (Figure 1, step 4). Steps 1 and 4 are therefore equivalent except that step 4 uses the supports produced by the previous synthesis cycle (steps 1 through 3) for codon synthesis whereas step 1 is the initial synthesis of the first codon in the oligonucleotide. The supports resulting from step 4 will each have two codons attached to them (i.e., a hexanucleotide) with the codon at the first position being any one of twenty possible codons (i.e., random) and the codon at the second position being one of the twenty possible codons.

For randomization of the codon at the second position and synthesis of the third position codon, steps 2 through 4 are again repeated. This process yields in each vessel a three codon oligonucleotide (i.e., 9 nucleotides) with codon positions 1 and 2 randomized and position three containing one of the twenty possible codons. Steps 2 through 4 are repeated to randomize the third position codon and synthesize the codon at the next position. The process is continued until an oligonucleotide of the desired length is achieved. After the final randomization step, the oligonucleotide can be cleaved from the supports and isolated by methods known to one skilled in the art. Alternatively, the oligonucleotides can remain on the supports for use in methods employing probe hybridization.

The diversity of codon sequences, i.e., the number of different possible oligonucleotides, that can be obtained using the methods of the present invention, is

extremely large and only limited by the physical characteristics of available materials. For example, a support composed of beads of about 100 μm in diameter will be limited to about 10,000 beads/reaction vessel using a 1 μm reaction vessel containing 25 mg of beads. This size bead can support about 1×10^7 oligonucleotides per bead. Synthesis using separate reaction vessels for each of the twenty amino acids will produce beads in which all the oligonucleotides attached to an individual bead are identical. The diversity which can be obtained under these conditions is approximately 10^7 copies of 10,000 x 20 or 200,000 different random oligonucleotides. The diversity can be increased, however, in several ways without departing from the basic methods disclosed herein. For example, the number of possible sequences can be increased by decreasing the size of the individual beads which make up the support. A bead of about 30 μm in diameter will increase the number of beads per reaction vessel and therefore the number of oligonucleotides synthesized. Another way to increase the diversity of oligonucleotides with random codons is to increase the volume of the reaction vessel. For example, using the same size bead, a larger volume can contain a greater number of beads than a smaller vessel and therefore support the synthesis of a greater number of oligonucleotides. Increasing the number of codons coupled to a support in a single reaction vessel also increases the diversity of the random oligonucleotides. The total diversity will be the number of codons coupled per vessel raised to the number of codon positions synthesized. For example, using ten reaction vessels, each synthesizing two codons to randomize a total of twenty codons, the number of different oligonucleotides of ten codons in length per 100 μm bead can be increased where each bead will contain about 2^{10} or 1×10^3 different sequences instead of one. One skilled in the art will know how to modify such parameters to increase the diversity of oligonucleotides with random codons.

A method of synthesizing oligonucleotides having random codons at each position using individual monomers wherein the number of reaction vessels is less than the number of codons to be randomized is also described. For example, if twenty codons are to be randomized at each position within an oligonucleotide population, then ten reaction vessels can be used. The use of a smaller number of reaction vessels than the number of codons to be randomized at each position is preferred because the smaller number of reaction vessels is easier to manipulate and results in a greater number of possible oligonucleotides synthesized.

The use of a smaller number of reaction vessels for random synthesis of twenty codons at a desired position within an oligonucleotide is similar to that described above using twenty reaction vessels except that each reaction vessel can contain the synthesis products of more than one codon. For example, step one synthesis using ten reaction vessels proceeds by coupling about two different codons on supports contained in each of ten reaction vessels. This is shown in Figure 2 where each of the two codons coupled to a different support can consist of the following sequences: (1) (T/G)TT for Phe and Val; (2) (T/C)CT for Ser and Pro; (3) (T/C)AT for Tyr and His; (4) (T/C)GT for Cys and Arg; (5) (C/A)TG for Leu and Met; (6) (C/G)AG for Gln and Glu; (7) (A/G)CT for Thr and Ala; (8) (A/G)AT for Asn and Asp; (9) (T/G)GG for Trp and Gly and (10) A(T/A)A for Ile and Cys. The slash (/) signifies that a mixture of the monomers indicated on each side of the slash are used as if they were a single monomer in the indicated coupling step. The antisense sequence for each of the above codons can be generated by synthesizing the complementary sequence. For example, the antisense for Phe and Val can be AA(C/A). The amino acids encoded by each of the above pairs of sequences are given as the standard three letter nomenclature.

Coupling of the monomers in this fashion will yield codons specifying all twenty of the naturally occurring amino acids attached to supports in ten reaction vessels. However, the number of individual reaction vessels to be used will depend on the number of codons to be randomized at the desired position and can be determined by one skilled in the art. For example, if ten codons are to be randomized, then five reaction vessels can be used for coupling. The codon sequences given above can be used for this synthesis as well. The sequences of the codons can also be changed to incorporate or be replaced by any of the additional forty-four codons which constitutes the genetic code.

The remaining steps of synthesis of oligonucleotides with random codons using a smaller number of reaction vessels are as outlined above for synthesis with twenty reaction vessels except that the mixing and dividing steps are performed with supports from about half the number of reaction vessels. These remaining steps are shown in Figure 2 (steps 2 through 4).

Oligonucleotides having at least one specified tuplet at a predetermined position and the remaining positions having random tuplets are synthesized using the methods described herein. The synthesis steps are similar to those outlined above using twenty or less reaction vessels except that prior to synthesis of the specified codon position, the dividing of the supports into separate reaction vessels for synthesis of different codons is omitted. For example, if the codon at the second position of the oligonucleotide is to be specified, then following synthesis of random codons at the first position and mixing of the supports, the mixed supports are not divided into new reaction vessels but, instead, are contained in a single reaction vessel to synthesize the specified codon. The specified codon is synthesized sequentially from

individual monomers as described above. Thus, the number of reaction vessels is increased or decreased at each step to allow for the synthesis of a specified codon or a desired number of random codons. In the most preferred
5 embodiment of this invention, the specified codons are codons capable of forming covalent bonds, e.g., cysteine, glutamic acid, lysine, leucine and tyrosine.

Following codon synthesis, the mixed supports are divided into individual reaction vessels for synthesis of
10 the next codon to be randomized (Figure 1, step 3) or can be used without separation for synthesis of a consecutive specified codon. The rounds of synthesis can be repeated for each codon to be added until the desired number of positions with predetermined or randomized codons are
15 obtained.

Synthesis of oligonucleotides with the first position codon being specified can also be synthesized using the above method. In this case, the first position codon is synthesized from the appropriate monomers. The
20 supports are divided into the required number of reaction vessels needed for synthesis of random codons at the second position and the rounds of synthesis, mixing and dividing are performed as described above.

A method of synthesizing oligonucleotides having
25 tuplets which are diverse but biased toward a predetermined sequence is also described herein. This method employs two reaction vessels, one vessel for the synthesis of a predetermined sequence and the second vessel for the synthesis of a random sequence. This method is
30 advantageous to use when a significant number of codon positions, for example, are to be of a specified sequence since it alleviates the use of multiple reaction vessels. Instead, a mixture of four different monomers such as adenine, guanine, cytosine and thymine nucleotides are used

for the first and second monomers in the codon. The codon is completed by coupling a mixture of a pair of monomers of either guanine and thymine or cytosine and adenine nucleotides at the third monomer position. In the second
5 vessel, nucleotide monomers are coupled sequentially to yield the predetermined codon sequence. Mixing of the two supports yields a population of oligonucleotides containing both the predetermined codon and the random codons at the desired position. Synthesis can proceed by using this
10 mixture of supports in a single reaction vessel, for example, for coupling additional predetermined codons or, further dividing the mixture into two reaction vessels for synthesis of additional random codons.

The two reaction vessel method can be used for
15 codon synthesis within an oligonucleotide with a predetermined tuplet sequence by dividing the support mixture into two portions at the desired codon position to be randomized. Additionally, this method allows for the extent of randomization to be adjusted. For example,
20 unequal mixing or dividing of the two supports will change the fraction of codons with predetermined sequences compared to those with random codons at the desired position. Unequal mixing and dividing of supports can be useful when there is a need to synthesize random codons at
25 a significant number of positions within an oligonucleotide of a longer or shorter length.

The extent of randomization can also be adjusted by using unequal mixtures of monomers in the first, second and third monomer coupling steps of the random codon
30 position. The unequal mixtures can be in any or all of the coupling steps to yield a population of codons enriched in sequences reflective of the monomer proportions.

Synthesis of randomized oligonucleotides is performed using methods well known to one skilled in the

art. Linear coupling of monomers can, for example, be accomplished using phosphoramidite chemistry with a MilliGen/Biosearch Cyclone Plus automated synthesizer as described by the manufacturer (Millipore, Burlington, MA).
5 Other chemistries and automated synthesizers can be employed as well and are known to one skilled in the art.

Synthesis of multiple codons can be performed without modification to the synthesizer by separately synthesizing the codons in individual sets of reactions.
10 Alternatively, modification of an automated DNA synthesizer can be performed for the simultaneous synthesis of codons in multiple reaction vessels.

In one embodiment, the invention provides a plurality of procaryotic cells containing a diverse
15 population of expressible oligonucleotides operationally linked to expression elements, the expressibl oligonucleotides having a desirable bias of random codon sequences. These oligonucleotides can, in one embodiment, be produced from diverse combinations of first and second
20 precursor oligonucleotides having a desirable bias of random sequences. The invention provides for a method for constructing such a plurality of procaryotic cells as well.

The oligonucleotides synthesized by the above methods can be used to express a plurality of random
25 soluble peptides having constrained secondary structure in solution, diverse but biased toward a predetermined sequence or which contain at least one specified codon at a predetermined position. The need will determine which type of oligonucleotide is to be expressed to give the
30 resultant population of random peptides and is known to one skilled in the art. Expression can be performed in any compatible vector/host system. Such systems include, for example, plasmids or phagemids in procaryotes such as E. coli, yeast systems, and other eucaryotic systems such as

mammalian cells, but will be described herein in context with its presently preferred embodiment, i.e. expression on the surface of filamentous bacteriophage. Filamentous bacteriophage can be, for example, M13, fl and fd. Such
5 phage have circular single-stranded genomes and double strand replicative DNA forms. Additionally, the peptides can also be expressed in soluble or secreted form depending on the need and the vector/host system employed. Furthermore, this invention provides host cells containing
10 the expressible oligonucleotides, the vectors and the isolated soluble, stable peptides produced by growing a host cell described above under conditions favoring expression of the oligonucleotide, and isolating the peptide so produced.

15 For the purpose of illustration only, expression of random peptides on the surface of M13 can be accomplished, for example, using the vector system shown in Figure 3. Construction of the vectors enabling one of ordinary skill to make them are explicitly set out in
20 Examples I and II. The complete nucleotide sequences are given in Figures 5, 6 and 7 (SEQ ID NOS: 1, 2 and 3, respectively). This system produces random oligonucleotides functionally linked to expression elements and to gVIII by combining two smaller oligonucleotide
25 portions contained in separate vectors into a single vector. The diversity of oligonucleotide species obtained by this system or others described herein can be 5×10^7 or greater. Diversity of less than 5×10^7 can also be obtained and will be determined by the need and type of
30 random peptides to be expressed. The random combination of two precursor portions into a larger oligonucleotide increases the diversity of the population several fold and has the added advantage of producing oligonucleotides larger than what can be synthesized by standard methods.
35 Additionally, although the correlation is not known, when the number of possible paths an oligonucleotide can take

during synthesis such as described herein is greater than the number of beads, then there will be a correlation between the synthesis path and the sequences obtained. By combining oligonucleotide populations which are synthesized
5 separately, this correlation will be destroyed. Therefore, any bias which may be inherent in the synthesis procedures will be alleviated by joining two precursor portions into a contiguous random oligonucleotide.

Populations of precursor oligonucleotides to be
10 combined into an expressible form are each cloned into separate vectors. The two precursor portions which make up the combined oligonucleotide corresponds to the carboxy and amino terminal portions of the expressed peptide. Each precursor oligonucleotide can encode either the sense or
15 anti-sense and will depend on the orientation of the expression elements and the gene encoding the fusion portion of the protein as well as the mechanism used to join the two precursor oligonucleotides. For the vectors shown in Figure 3, precursor oligonucleotides corresponding
20 to the carboxy terminal portion of the peptide encode the sense strand. Those corresponding to the amino terminal portion encode the anti-sense strand. Oligonucleotide populations are inserted between the Eco RI and Sac I restriction enzyme sites in M13IX22 and M13IX42 (Figure 3A and B). M13IX42 (SEQ ID NO: 1) is the vector used for
25 sense strand precursor oligonucleotide portions and M13IX22 (SEQ ID NO: 2) is used for anti-sense precursor portions.

The populations of randomized oligonucleotides inserted into the vectors are synthesized with Eco RI and
30 Sac I recognition sequences flanking opposite ends of the random codon sequences. The sites allow annealing and ligation of these single strand oligonucleotides into a double stranded vector restricted with Eco RI and Sac I. Alternatively, the oligonucleotides can be inserted into
35 the vector by standard mutagenesis methods. In this latter

method, single stranded vector DNA is isolated from the phage and annealed with random oligonucleotides having known sequences complementary to vector sequences. The oligonucleotides are extended with DNA polymerase to
5 produce double stranded vectors containing the randomized oligonucleotides.

A vector useful for sense strand oligonucleotide portions, M13IX42 (Figure 3B) contains down-stream and in frame with the Eco RI and Sac I restriction sites a
10 sequence encoding the pseudo-wild type gVIII product. This gene encodes the wild type M13 gVIII amino acid sequence but has been changed at the nucleotide level to reduce homologous recombination with the wild type gVIII contained on the same vector. The wild type gVIII is present to
15 ensure that at least some functional, non-fusion coat protein will be produced. The inclusion of a wild type gVIII therefore reduces the possibility of non-viable phage production and biological selection against certain peptide fusion proteins. Differential regulation of the two genes
20 can also be used to control the relative ratio of the pseudo and wild type proteins.

Also contained downstream and in frame with the Eco RI and Sac I restriction sites is an amber stop codon. The mutation is located six codons downstream from Sac I
25 and therefore lies between the inserted oligonucleotides and the gVIII sequence. As was the function of the wild type gVIII, the amber stop codon also reduces biological selection when combining precursor portions to produce expressible oligonucleotides. This is accomplished by
30 using a non-suppressor (sup O) host strain because non-suppressor strains will terminate expression after the oligonucleotide sequences but before the pseudo gVIII sequences. Therefore, the pseudo gVIII will never be expressed on the phage surface under these circumstances.
35 Instead, only soluble peptides will be produced.

Expression in a non-suppressor strain can be advantageously utilized when one wishes to produce large populations of soluble peptides. Stop codons other than amber, such as opal and ochre, or molecular switches, such as inducible
5 repressor elements, can also be used to unlink peptide expression from surface expression. Additional controls exist as well and are described below.

A vector useful for anti-sense strand oligonucleotide portions, M13IX22, (Figure 3A), contains
10 the expression elements for the peptide fusion proteins. Upstream and in frame with the Sac I and Eco RI sites in this vector is a leader sequence for surface expression. A ribosome binding site and Lac Z promoter/operator elements are present for transcription and translation of
15 the peptide fusion proteins.

Both vectors contain a pair of Fok I restriction enzyme sites (Figure 3 A and B) for joining together two precursor oligonucleotide portions and their vector sequences. One site is located at the ends of each
20 precursor oligonucleotide which is to be joined. The second Fok I site within the vectors is located at the end of the vector sequences which are to be joined. The 5' overhang of this second Fok I site has been altered to encode a sequence which is not found in the overhangs
25 produced at the first Fok I site within the oligonucleotide portions. The two sites allow the cleavage of each circular vector into two portions and subsequent ligation of essential components within each vector into a single circular vector where the two oligonucleotide precursor
30 portions form a contiguous sequence (Figure 3C). Non-compatible overhangs produced at the two Fok I sites allows optimal conditions to be selected for performing concatemerization or circularization reactions for joining the two vector portions. Such selection of conditions can
35 be used to govern the reaction order and therefore increase

the efficiency of joining.

Fok I is a restriction enzyme whose recognition sequence is distal to the point of cleavage. Distal placement of the recognition sequence in its location to the cleavage point is important since if the two were superimposed within the oligonucleotide portions to be combined, it would lead to an invariant codon sequence at the juncture. To alleviate the formation of invariant codons at the juncture, Fok I recognition sequences can be placed outside of the random codon sequence and still be used to restrict within the random sequence. Subsequent annealing of the single-strand overhangs produced by Fok I and ligation of the two oligonucleotide precursor portions allows the juncture to be formed. A variety of restriction enzymes restrict DNA by this mechanism and can be used instead of Fok I to join precursor oligonucleotides without creating invariant codon sequences. Such enzymes include, for example, Alw I, Bbu I, Bsp MI, Hga I, Eph I, Mbo II, Mnl I, Ple I and Sfa NI. One skilled in the art knows how to substitute Fok I recognition sequences for alternative enzyme recognition sequences such as those above, and use the appropriate enzyme for joining precursor oligonucleotide portions.

Although the sequences of the precursor oligonucleotides are random and will invariably have oligonucleotides within the two precursor populations whose sequences are sufficiently complementary to anneal after cleavage, the efficiency of annealing can be increased by insuring that the single-strand overhangs within one precursor population will have a complementary sequence within the second precursor population. This can be accomplished by synthesizing a non-degenerate series of known sequences at the Fok I cleavage site coding for each of the twenty amino acids. Since the Fok I cleavage site contains a four base overhang, forty different sequences

are needed to randomly encode all twenty amino acids. For example, if two precursor populations of ten codons in length are to be combined, then after the ninth codon position is synthesized, the mixed population of supports
5 are divided into forty reaction vessels for each of the populations and complementary sequences for each of the corresponding reaction vessels between populations are independently synthesized. The sequences are shown in Tables III and VI of Example I where the oligonucleotides
10 on columns 1R through 40R form complementary overhangs with the oligonucleotides on the corresponding columns 1L through 40L once cleaved. The degenerate X positions in Table VI are necessary to maintain the reading frame once the precursor oligonucleotide portions are joined.
15 However, use of restriction enzymes which produce a blunt end, such as Mnl I can be alternatively used in place of Fok I to alleviate the degeneracy introduced in maintaining the reading frame.

The last feature exhibited by each of the vectors
20 is an amber stop codon located in an essential coding sequence within the vector portion lost during combining (Figure 3C). The amber stop codon is present to select for viable phage produced from only the proper combination of precursor oligonucleotides and their vector sequences into
25 a single vector species. Other non-sense mutations or selectable markers can work as well.

The combining step randomly brings together different precursor oligonucleotides within the two populations into a single vector (Figure 3C; M13IX). For
30 example, the vector sequences donated from each independent vector described above, M13IX22 and M13IX42, are necessary for production of viable phage. Also, since the expression elements are contained in M13IX22 and the gVIII sequences are contained in M13IX42, expression of functional gVIII-
35 peptide fusion proteins cannot be accomplished until the

sequences are linked as shown in M13IX.

The combining step is performed by restricting each population of vectors containing randomized oligonucleotides with Fok I, mixing and ligating (Figure 3C). Any vectors generated which contain an amber stop codon will not produce viable phage when introduced into a non-suppressor strain (Figure 3D). Therefore, only the sequences which do not contain an amber stop codon will make up the final population of vectors contained in the library. These vector sequences are the sequences required for surface expression of randomized peptides. By analogous methodology, more than two vector portions can be combined into a single vector which expresses random peptides.

Surface expression of the random peptide library is performed in an amber suppressor strain. As described above, the amber stop codon between the random codon sequence and the gVIII sequence unlinks the two components in a non-suppressor strain. Isolating the phage produced from the non-suppressor strain and infecting a suppressor strain will link the random codon sequences to the gVIII sequence during expression (Figure 3E). Culturing the suppressor strain after infection allows the expression of all peptide species within the library as gVIII-peptide fusion proteins. Alternatively, the DNA can be isolated from the non-suppressor strain and then introduced into a suppressor strain to accomplish the same effect.

The level of expression of gVIII-peptide fusion proteins can additionally be controlled at the transcriptional level. The gVIII-peptide fusion proteins are under the inducible control of the Lac 2 promoter/operator system. Other inducible promoters can work as well and are known by one skilled in the art. For high levels of surface expression, the suppressor library

is cultured in an inducer of the Lac Z promoter such as isopropylthio- β -galactoside (IPTG). Inducible control is beneficial because biological selection against non-functional gVIII-peptide fusion proteins can be minimized
5 by culturing the library under non-expressing conditions. Expression can then be induced only at the time of screening to ensure that the entire population of oligonucleotides within the library are accurately represented on the phage surface. Also this can be used to
10 control the valency of the peptide on the phage surface.

The surface expression library is screened for specific peptides which bind ligand binding proteins by standard affinity isolation procedures. Such methods include, for example, panning, affinity chromatography and
15 solid phase blotting procedures. Panning as described by Parmley and Smith, Gene 73:305-318 (1988), which is incorporated herein by reference, is preferred because high titers of phage can be screened easily, quickly and in small volumes. Furthermore, this procedure can select
20 minor peptide species within the population, which otherwise would have been undetectable, and amplified to substantially homogenous populations. The selected peptide sequences can be determined by sequencing the nucleic acid encoding such peptides after amplification of the phage
25 population.

The invention provides a plurality of procaryotic cells containing a diverse population of oligonucleotides encoding soluble peptides having constrained secondary structure in solution, the oligonucleotides being
30 operationally linked to expression sequences. The invention provides for methods of constructing such populations of cells as well.

Random oligonucleotides synthesized by any of the methods described previously can also be expressed on the

surface of filamentous bacteriophage, such as M13, for example, without the joining together of precursor oligonucleotides. A vector such as that shown in Figure 4, M13IX30, can be used. This vector exhibits all the functional features of the combined vector shown in Figure 3C for surface expression of gVIII-peptide fusion proteins. The complete nucleotide sequence for M13IX30 (SEQ ID NO: 3) is shown in Figure 7.

For example, M13IX30 contains a wild type gVIII for phage viability and a pseudo gVIII sequence for peptide fusions. The vector also contains in frame restriction sites for cloning random peptides. The cloning sites in this vector are Xho I, Stu I and Spe I. Oligonucleotides should therefore be synthesized with the appropriate complementary ends for annealing and ligation or insertional mutagenesis. Alternatively, the appropriate termini can be generated by PCR technology. Between the restriction sites and the pseudo gVIII sequence is an in-frame amber stop codon, again, ensuring complete viability of phage in constructing and manipulating the library. Expression and screening is performed as described above for the surface expression library of oligonucleotides generated from precursor portions.

Thus, peptides can be selected that are capable of being bound by a ligand binding protein from a population of random peptides by (a) operationally linking a diverse population of oligonucleotides having a desirable bias of random codon sequences to expression elements; (b) introducing said population of vectors into a compatible host under conditions sufficient for expressing said population of random peptides; and (c) determining the peptides which bind to said binding protein. Also provided is a method for determining the encoding nucleic acid sequence of such selected peptides.

The following examples are intended to illustrate, but not limit the invention.

EXAMPLE I

5 Isolation and Characterization of Peptide Ligands Generated From Right and Left Half Random Oligonucleotides

This example shows the synthesis of random oligonucleotides and the construction and expression of surface expression libraries of the encoded randomized
10 peptides. The random peptides of this example derive from the mixing and joining together of two random oligonucleotides. Also demonstrated is the isolation and characterization of peptide ligands and their corresponding nucleotide sequence for specific binding proteins.

15 Synthesis of Random Oligonucleotides

The synthesis of two randomized oligonucleotides which correspond to smaller portions of a larger randomized oligonucleotide is shown below. Each of the two smaller portions make up one-half of the larger oligonucleotide.
20 The population of randomized oligonucleotides constituting each half are designated the right and left half. Each population of right and left halves are ten codons in length with twenty random codons at each position. The right half corresponds to the sense sequence of the
25 randomized oligonucleotides and encode the carboxy terminal half of the expressed peptides. The left half corresponds to the anti-sense sequence of the randomized oligonucleotides and encode the amino terminal half of the expressed peptides. The right and left halves of the
30 randomized oligonucleotide populations are cloned into separate vector species and then mixed and joined so that the right and left halves come together in random combination to produce a single expression vector species

which contains a population of randomized oligonucleotides twenty codons in length. Electroporation of the vector population into an appropriate host produces filamentous phage which express the random peptides on their surface.

5 The reaction vessels for oligonucleotide synthesis were obtained from the manufacturer of the automated synthesizer (Millipore, Burlington, MA; supplier of MilliGen/Biosearch Cyclone Plus Synthesizer). The vessels were supplied as packages containing empty reaction
10 columns (1 μ mole), frits, crimps and plugs (MilliGen/Biosearch catalog # GEN 860458). Derivatized and underivatized control pore glass, phosphoramidite nucleotides, and synthesis reagents were also obtained from MilliGen/Biosearch. Crimper and decrimper tools were
15 obtained from Fisher Scientific Co., Pittsburgh, PA (Catalog numbers 06-406-20 and 06-406-25A, respectively).

Ten reaction columns were used for right half synthesis of random oligonucleotides ten codons in length. The oligonucleotides have 5 monomers at their 3' end of the
20 sequence 5'GAGCT3' and 8 monomers at their 5' end of the sequence 5'AATTCCAT3'. The synthesizer was fitted with a column derivatized with a thymine nucleotide (T-column, MilliGen/Biosearch # 0615.50) and was programmed to synthesize the sequences shown in Table I for each of ten
25 columns in independent reaction sets. The sequence of the last three monomers (from right to left since synthesis proceeds 3' to 5') encode the indicated amino acids:

Table I

30	<u>Column</u>	<u>Sequence</u> <u>(5' to 3')</u>	<u>Amino Acids</u>
	column 1R	(T/G)TTGAGCT	Phe and Val
	column 2R	(T/C)CTGAGCT	Ser and Pro
	column 3R	(T/C)ATGAGCT	Tyr and His

	column 4R	(T/C)GTGAGCT	Cys and Arg
	column 5R	(C/A)TGGAGCT	Leu and Met
	column 6R	(C/G)AGGAGCT	Gln and Glu
	column 7R	(A/G)CTGAGCT	Thr and Ala
5	column 8R	(A/G)ATGAGCT	Asn and Asp
	column 9R	(T/G)GGGAGCT	Trp and Gly
	column 1R	A(T/A)AGAGCT	Ile and Cys

where the two monomers in parentheses denote a single monomer position within the codon and indicate that an equal mixture of each monomer was added to the reaction for coupling. The monomer coupling reactions for each of the 10 columns were performed as recommended by the manufacturer (amidite version S1.06, # 8400-050990, scale 1 μ M). After the last coupling reaction, the columns were washed with acetonitrile and lyophilized to dryness.

Following synthesis, the plugs were removed from each column using a decrimper and the reaction products were poured into a single weigh boat. Initially the bead mass increases, due to the weight of the monomers, however, at later rounds of synthesis material is lost. In either case, the material was equalized with underivatized control pore glass and mixed thoroughly to obtain a random distribution of all twenty codon species. The reaction products were then aliquotted into 10 new reaction columns by removing 25 mg of material at a time and placing it into separate reaction columns. Alternatively, the reaction products can be aliquotted by suspending the beads in a liquid that is dense enough for the beads to remain dispersed, preferably a liquid that is equal in density to the beads, and then aliquoting equal volumes of the suspension into separate reaction columns. The lip on the inside of the columns where the frits rest was cleared of material using vacuum suction with a syringe and 25 G needle. New frits were placed onto the lips, the plugs were fitted into the columns and were crimped into place

using a crimper.

Synthesis of the second codon position was achieved using the above 10 columns containing the random mixture of reaction products from the first codon synthesis. The monomer coupling reactions for the second codon position are shown in Table II. An A in the first position means that any monomer can be programmed into the synthesizer. At that position, the first monomer position is not coupled by the synthesizer since the software assumes that the monomer is already attached to the column. An A also denotes that the columns from the previous codon synthesis should be placed on the synthesizer for use in the present synthesis round. Reactions were again sequentially repeated for each column as shown in Table II and the reaction products washed and dried as described above.

Table II

	<u>Column</u>	<u>Sequence (5' to 3')</u>	<u>Amino Acids</u>
5	column 1R	(T/G)TTA	Phe and Val
	column 2R	(T/C)CTA	Ser and Pro
	column 3R	(T/C)ATA	Tyr and His
	column 4R	(T/C)GTA	Cys and Arg
	column 5R	(C/A)TGA	Leu and Met
10	column 6R	(C/G)AGA	Gln and Glu
	column 7R	(A/G)CTA	Thr and Ala
	column 8R	(A/G)ATA	Asn and Asp
	column 9R	(T/G)GGA	Trp and Gly
	column 10R	A(T/A)AA	Ile and Cys

Randomization of the second codon position was achieved by removing the reaction products from each of the columns and thoroughly mixing the material. The material was again divided into new reaction columns and prepared for monomer coupling reactions as described above.

Random synthesis of the next seven codons (positions 3 through 9) proceeded identically to the cycle described above for the second codon position and again used the monomer sequences of Table II. Each of the newly repacked columns containing the random mixture of reaction products from synthesis of the previous codon position was used for the synthesis of the subsequent codon position. After synthesis of the codon at position nine and mixing of the reaction products, the material was divided and repacked into 40 different columns and the monomer sequences shown in Table III were coupled to each of the 40 columns in independent reactions. The oligonucleotides from each of the 40 columns were mixed once more and elaved from the control pore glass as recommended by the manufacturer.

Table III

	<u>Column</u>	<u>Sequence (5' to 3')</u>
5	column 1R	AATTCTTTTA
	column 2R	AATTCTGTTA
	column 3R	AATTCGTTTA
	column 4R	AATTCGGTTA
	column 5R	AATTCTTCTA
10	column 6R	AATTCTCCTA
	column 7R	AATTCGTCTA
	column 8R	AATTCGCCTA
	column 9R	AATTCTTATA
	column 10R	AATTCTCATA
15	column 11R	AATTCGTATA
	column 12R	AATTCGCATA
	column 13R	AATTCTTGTA
	column 14R	AATTCTCGTA
	column 15R	AATTCGTGTA
20	column 16R	AATTCGCGTA
	column 17R	AATTCTCTGA
	column 18R	AATTCTATGA
	column 19R	AATTCGCTGA
	column 20R	AATTCGATGA
25	column 21R	AATTCTCAGA
	column 22R	AATTCTGAGA
	column 23R	AATTCGCAGA
	column 24R	AATTCGGAGA
	column 25R	AATTCTACTA
30	column 26R	AATTCTGCTA
	column 27R	AATTCGACTA
	column 28R	AATTCGGCTA
	column 29R	AATTCTAATA
	column 30R	AATTCTGATA
35	column 31R	AATTCGAATA
	column 32R	AATTCGGATA
	column 33R	AATTCTTGCA
	column 34R	AATTCTGGGA

35

	column 35R	<u>AATTCGTGGA</u>
	column 36R	<u>AATTCGGGGA</u>
	column 37R	<u>AATTCTATAA</u>
	column 38R	<u>AATTCTAAAA</u>
5	column 39R	<u>AATTCGATAA</u>
	column 40R	<u>AATTCGAAAA</u>

Left half synthesis of random oligonucleotides proceeded similarly to the right half synthesis. This half of the oligonucleotide corresponds to the anti-sense sequence of the encoded randomized peptides. Thus, the complementary sequence of the codons in Tables I through III are synthesized. The left half oligonucleotides also have 5 monomers at their 3' end of the sequence 5'GAGCT3' and 8 monomers at their 5' end of the sequence 5'AATTCAT3'. The rounds of synthesis, washing, drying, mixing, and dividing are as described above.

For the first codon position, the synthesizer was fitted with a T-column and programmed to synthesize the sequences shown in Table IV for each of ten columns in independent reaction sets. As with right half synthesis, the sequence of the last three monomers (from right to left) encode the indicated amino acids:

Table IV

	<u>Column</u>	<u>Sequence (5' to 3')</u>	<u>Amino Acids</u>
5	column 1L	AA(A/C)GAGCT	Phe and Val
	column 2L	AG(A/G)GAGCT	Ser and Pro
	column 3L	AT(A/G)GAGCT	Tyr and His
	column 4L	AC(A/G)GAGCT	Cys and Arg
	column 5L	CA(G/T)GAGCT	Leu and Met
10	column 6L	CT(G/C)GAGCT	Gln and Glu
	column 7L	AG(T/C)GAGCT	Thr and Ala
	column 8L	AT(T/C)GAGCT	Asn and Asp
	column 9L	CC(A/C)GAGCT	Trp and Gly
	column 10L	T(A/T)TGAGCT	Ile and Cys

Following washing and drying, the plugs for each
 15 column were removed, mixed and aliquotted into ten new
 reaction columns as described above. Synthesis of the
 second codon position was achieved using these ten columns
 containing the random mixture of reaction products from the
 first codon synthesis. The monomer coupling reactions for
 20 the second codon position are shown in Table V.

Table V

	<u>Column</u>	<u>Sequence (5' to 3')</u>	<u>Amino Acids</u>
25	column 1L	AA(A/C) <u>A</u>	Phe and Val
	column 2L	AG(A/G) <u>A</u>	Ser and Pro
	column 3L	AT(A/G) <u>A</u>	Tyr and His
	column 4L	AC(A/G) <u>A</u>	Cys and Arg
	column 5L	CA(G/T) <u>A</u>	Leu and Met
30	column 6L	CT(G/C) <u>A</u>	Gln and Glu
	column 7L	AG(T/C) <u>A</u>	Thr and Ala
	column 8L	AT(T/C) <u>A</u>	Asn and Asp
	column 9L	CC(A/C) <u>A</u>	Trp and Gly
	column 10L	T(A/T) <u>TA</u>	Ile and Cys

Again, randomization of the second codon position was achieved by removing the reaction products from each of the columns and thoroughly mixing the beads. The beads were repacked into ten new reaction columns.

5 Random synthesis of the next seven codon positions proceeded identically to the cycle described above for the second codon position and again used the monomer sequences of Table V. After synthesis of the codon at position nine and mixing of the reaction products, the
10 material was divided and repacked into 40 different columns and the monomer sequences shown in Table VI were coupled to each of the 40 columns in independent reactions.

Table VI

15	<u>Column</u>	<u>Sequence (5' to 3')</u>
	column 1L	AATTCCATAAAAXXA
	column 2L	AATTCCATAAACXXA
	column 3L	AATTCCATAACAXXA
	column 4L	AATTCCATAACCXXA
20	column 5L	AATTCCATAGAAXXA
	column 6L	AATTCCATAGACXXA
	column 7L	AATTCCATAGGAXXA
	column 8L	AATTCCATAGGCXXA
	column 9L	AATTCCATATAAXXA
25	column 10L	AATTCCATATACXXA
	column 11L	AATTCCATATGAXXA
	column 12L	AATTCCATATGCXXA
	column 13L	AATTCCATACAAXXA
	column 14L	AATTCCATACACXXA
30	column 15L	AATTCCATACGAXXA
	column 16L	AATTCCATACGCXXA
	column 17L	AATTCCATCAGAXXA
	column 18L	AATTCCATCAGCXXA
	column 19L	AATTCCATCATAXXA
35	column 20L	AATTCCATCATCXXA

	column 21L	AATTCCATCTGAXXA
	column 22L	AATTCCATCTGCXXA
	column 23L	AATTCCATCTCAXXA
	column 24L	AATTCCATCTCCXXA
5	column 25L	AATTCCATAGTAXXA
	column 26L	AATTCCATAGTCXXA
	column 27L	AATTCCATAGCAXXA
	column 28L	AATTCCATAGCCXXA
	column 29L	AATTCCATATTAXXA
10	column 30L	AATTCCATATTCXXA
	column 31L	AATTCCATATCAXXA
	column 32L	AATTCCATATCCXXA
	column 33L	AATTCCATCCAAXXA
	column 34L	AATTCCATCCACXXA
15	column 35L	AATTCCATCCCAXXA
	column 36L	AATTCCATCCCCXXA
	column 37L	AATTCCATTATAAXXA
	column 38L	AATTCCATTATCXXA
	column 39L	AATTCCATTTTAXXA
20	column 40L	AATTCCATTTTCXXA

The first two monomers denoted by an "X" represent an equal mixture of all four nucleotides at that position. This is necessary to retain a relatively unbiased codon sequence at the junction between right and left half oligonucleotides.

25 The above right and left half random oligonucleotides were cleaved and purified from the supports and used in constructing the surface expression libraries below.

Vector Construction

Two M13-based vectors, M13IX42 (SEQ ID NO: 1) and
 30 M13IX22 (SEQ ID NO: 2), were constructed for the cloning and propagation of right and left half populations of random oligonucleotides, respectively. The vectors were specially constructed to facilitate the random joining and subsequent expression of right and left half

oligonucleotide populations. Each vector within the population contains one right and one left half oligonucleotide from the population joined together to form a single contiguous oligonucleotide with random codons which is twenty-two codons in length. The resultant population of vectors are used to construct a surface expression library.

M13IX42, or the right-half vector, was constructed to harbor the right half populations of randomized oligonucleotides. M13mp18 (Pharmacia, Piscataway, NJ) was the starting vector. This vector was genetically modified to contain, in addition to the encoded wild type M13 gene VIII already present in the vector: (1) a pseudo-wild type M13 gene VIII sequence with a stop codon (amber) placed between it and an Eco RI-Sac I cloning site for randomized oligonucleotides; (2) a pair of Fok I sites to be used for joining with M13IX22, the left-half vector; (3) a second amber stop codon placed on the opposite side of the vector than the portion being combined with the left-half vector; and (4) various other mutations to remove redundant restriction sites and the amino terminal portion of Lac Z.

The pseudo-wild type M13 gene VIII was used for surface expression of random peptides. The pseudo-wild type gene encodes the identical amino acid sequence as that of the wild type gene; however, the nucleotide sequence has been altered so that only 63% identity exists between this gene and the encoded wild type gene VIII. Modification of the gene VIII nucleotide sequence used for surface expression reduces the possibility of homologous recombination with the wild type gene VIII contained on the same vector. Additionally, the wild type M13 gene VIII was retained in the vector system to ensure that at least some functional, non-fusion coat protein would be produced. The inclusion of wild type gene VIII therefore reduces the

possibility of non-viable phage production from the random peptide fusion genes.

The pseudo-wild type gene VIII was constructed by chemically synthesizing a series of oligonucleotides which
5 encode both strands of the gene. The oligonucleotides are presented in Table VII (SEQ ID NOS: 7 through 16).

TABLE VII

Pseudo-Wild Type Gene VIII Oligonucleotide Series

10	<u>Top Strand</u> <u>Oligonucleotides</u>	<u>Sequence (5' to 3')</u>
	VIII 03	GATCC TAG GCT GAA GGC GAT GAC CCT GCT AAG GCT GC
	VIII 04	A TTC AAT AGT TTA CAG GCA AGT GCT ACT GAG TAC A
15	VIII 05	TT GGC TAC GCT TGG GCT ATG GTA GTA GTT ATA GTT
	VIII 06	GGT GCT ACC ATA GGG ATT AAA TTA TTC AAA AAG TT
	VIII 07	T ACG AGC AAG GCT TCT TA
20	<u>Bottom Strand</u> <u>Oligonucleotides</u>	
	VIII 08	AGC TTA AGA AGC CTT GCT CGT AAA CTT TTT GAA TAA TTT
	VIII 09	AAT CCC TAT GGT AGC ACC AAC TAT AAC TAC TAC CAT
25	VIII 10	AGC CCA AGC GTA GCC AAT GTA CTC AGT AGC ACT TG
	VIII 11	C CTG TAA ACT ATT GAA TGC AGC CTT AGC AGG GTC
30	VIII 12	ATC GCC TTC AGC CTA G

Except for the terminal oligonucleotides VIII 03 (SEQ ID NO: 7) and VIII 08 (SEQ ID NO: 12), the above oligonucleotides (oligonucleotides VIII 04-VIII 07 and 09-12 (SEQ ID NOS: 8 through 11 and 13 through 16)) were mixed at 200 ng each in 10 μ l final volume and phosphorylated with T4 polynucleotide Kinase (Pharmacia, Piscataway, NJ) with 1 mM ATP at 37°C for 1 hour. The reaction was stopped at 65°C for 5 minutes. Terminal oligonucleotides were added to the mixture and annealed into double-stranded form by heating to 65°C for 5 minutes, followed by cooling to room temperature over a period of 30 minutes. The annealed oligonucleotides were ligated together with 1.0 U of T4 DNA ligase (BRL). The annealed and ligated oligonucleotides yield a double-stranded DNA flanked by a Bam HI site at its 5' end and by a Hind III site at its 3' end. A translational stop codon (amber) immediately follows the Bam HI site. The gene VIII sequence begins with the codon GAA (Glu) two codons 3' to the stop codon. The double-stranded insert was phosphorylated using T4 DNA Kinase (Pharmacia, Piscataway, NJ) and ATP (10 mM Tris-HCl, pH 7.5, 10 mM MgCl₂) and cloned in frame with the Eco RI and Sac I sites within the M13 polylinker. To do so, M13mp18 was digested with Bam HI (New England Biolabs, Beverly, MA) and Hind III (New England Biolabs) and combined at a molar ratio of 1:10 with the double-stranded insert. The ligations were performed at 16°C overnight in 1X ligase buffer (50 mM Tris-HCl, pH 7.8, 10 mM MgCl₂, 20 mM DTT, 1 mM ATP, 50 μ g/ml BSA) containing 1.0 U of T4 DNA ligase (New England Biolabs). The ligation mixture was transformed into a host and screened for positive clones using standard procedures in the art.

Several mutations were generated within the right-half vector to yield functional M13IX42. The mutations were generated using the method of Kunkel et al., Meth. Enzymol. 154:367-382 (1987), which is incorporated herein by reference, for site-directed mutagenesis. The

reagents, strains and protocols were obtained from a Bio Rad Mutagenesis kit (Bio Rad, Richmond, CA) and mutagenesis was performed as recommended by the manufacturer.

A Fok I site used for joining the right and left halves was generated 8 nucleotides 5' to the unique Eco RI site using the oligonucleotide 5'-CTCGAATTCGTACATCCTGGTCATAGC-3' (SEQ ID NO: 17). The second Fok I site retained in the vector is naturally encoded at position 3547; however, the sequence within the overhang was changed to encode CTTC. Two Fok I sites were removed from the vector at positions 239 and 7244 of M13mpl8 as well as the Hind III site at the end of the pseudo gene VIII sequence using the mutant oligonucleotides 5'-CATTTTGCAGATGGCTTAGA-3' (SEQ ID NO: 18) and 5'-TAGCATTAAACGTCCAATA-3' (SEQ ID NO: 19), respectively. New Hind III and Mlu I sites were also introduced at position 3919 and 3951 of M13IX42. The oligonucleotides used for this mutagenesis had the sequences 5'-ATATATTTTAGTAAGCTTCATCTTCT-3' (SEQ ID NO: 20) and 5'-GACAAAGAACGCGTGAAACTTT-3' (SEQ ID NO: 21), respectively. The amino terminal portion of Lac Z was deleted by oligonucleotide-directed mutagenesis using the mutant oligonucleotide 5'-GCGGGCCTCTTCGCTATTGCTTAAGAAGCCTTGCT-3' (SEQ ID NO: 22). This deletion also removed a third M13mpl8 derived Fok I site. The distance between the Eco RI and Sac I sites was increased to ensure complete double digestion by inserting a spacer sequence. The spacer sequence was inserted using the oligonucleotide 5'-TTCAGCCTAGGATCCGCCGAGCTCTCCTACCTGCGAATTCGTACATCC-3' (SEQ ID NO: 23). Finally, an amber stop codon was placed at position 4492 using the mutant oligonucleotide 5'-TGGATTATACTTCTAAATAATGGA-3' (SEQ ID NO: 24). The amber stop codon is used as a biological selection to ensure the proper recombination of vector sequences to bring together right and left halves of the randomized oligonucleotides. In constructing the above mutations, all changes made in a

M13 coding region were performed such that the amino acid sequence remained unaltered. It should be noted that several mutations within M13mp18 were found which differed from the published sequence. Where known, these sequence differences are recorded herein as found and therefore may not correspond exactly to the published sequence of M13mp18.

The sequence of the resultant vector, M13IX42, is shown in Figure 5 (SEQ ID NO: 1). Figure 3A also shows M13IX42 where each of the elements necessary for producing a surface expression library between right and left half randomized oligonucleotides is marked. The sequence between the two Fok I sites shown by the arrow is the portion of M13IX42 which is to be combined with a portion of the left-half vector to produce random oligonucleotides as fusion proteins of gene VIII.

M13IX22, or the left-half vector, was constructed to harbor the left half populations of randomized oligonucleotides. This vector was constructed from M13mp19 (Pharmacia, Piscataway, NJ) and contains: (1) Two Fok I sites for mixing with M13IX42 to bring together the left and right halves of the randomized oligonucleotides; (2) sequences necessary for expression such as a promoter and signal sequence and translation initiation signals; (3) an Eco RI-Sac I cloning site for the randomized oligonucleotides; and (4) an amber stop codon for biological selection in bringing together right and left half oligonucleotides.

Of the two Fok I sites used for mixing M13IX22 with M13IX42, one is naturally encoded in M13mp18 and M13mp19 (at position 3547). As with M13IX42, the overhang within this naturally occurring Fok I site was changed to CTTC. The other Fok I site was introduced after construction of the translation initiation signals by site-

directed mutagenesis using the oligonucleotide 5'-TAACACTCATTCCGGATGGAATTCTGGAGTCTGGGT-3' (SEQ ID NO: 25).

The translation initiation signals were constructed by annealing of overlapping oligonucleotides as described above to produce a double-stranded insert containing a 5' Eco RI site and a 3' Hind III site. The overlapping oligonucleotides are shown in Table VIII (SEQ ID NOS: 26 through 34) and were ligated as a double-stranded insert between the Eco RI and Hind III sites of M13mp18 as described for the pseudo gene VIII insert. The ribosome binding site (AGGAGAC) is located in oligonucleotide 015 (SEQ ID NO: 26) and the translation initiation codon (ATG) is the first three nucleotides of oligonucleotide 016 (SEQ ID NO: 27).

15

TABLE VIII

Oligonucleotide Series for Construction of
Translation Signals in M13IX22

	<u>Oligonucleotide</u>	<u>Sequence (5' to 3')</u>
	015	AATT C GCC AAG GAG ACA GTC AT
20	016	AATG AAA TAC CTA TTG CCT ACG GCA GCC GCT GGA TTG TT
	017	ATTA CTC GCT GCC CAA CCA GCC ATG GCC GAG CTC GTG AT
25	018	GACC CAG ACT CCA GATATC CAA CAG GAA TGA GTG TTA AT
	019	TCT AGA ACG CGT C
	020	ACGT G ACG CGT TCT AGA AT TAA CACTCA TTC CTG T
30	021	TG GAT ATC TGG AGT CTG GGT CAT CAC GAG CTC GGC CAT G
	022	GC TGG TTG GGC AGC GAG TAA TAA CAA TCC AGC GGC TGC C

45

023

GT AGG CAA TAG GTA TTT CAT TAT
GAC TGT CCT TGG CG

- Oligonucleotide 017 (SEQ ID NO: 27) contained a Sac I restriction site 67 nucleotides downstream from the ATG codon. The naturally occurring Eco RI site was removed and a new site introduced 25 nucleotides downstream from the Sac I. Oligonucleotides 5'-TGACTGTCTCCTTGGCGTGTGAAATTGTTA-3' (SEQ ID NO: 35) and 5'-TAACACTCATTCCTGGATGGAATTCTGGAGTCTGGGT-3' (SEQ ID NO: 36) were used to generate each of the mutations, respectively. An amber stop codon was also introduced at position 3263 of M13mpl8 using the oligonucleotide 5'-CAATTTTATCCTAAATCTTACCAAC-3' (SEQ ID NO: 37).
- In addition to the above mutations, a variety of other modifications were made to remove certain sequences and redundant restriction sites. The LAC Z ribosome binding site was removed when the original Eco RI site in M13mpl8 was mutated. Also, the Fok I sites at positions 239, 6361 and 7244 of M13mpl8 were likewise removed with mutant oligonucleotides 5'-CATTTTTGCAGATGGCTTAGA-3' (SEQ ID NO: 38), 5'-CGAAAGGGGGGTGTGCTGCAA-3' (SEQ ID NO: 39) and 5'-TAGCATTAACGTCCAATA-3' (SEQ ID NO: 40), respectively. Again, mutations within the coding region did not alter the amino acid sequence.

- The resultant vector, M13IX22, is 7320 base pairs in length, the sequence of which is shown in Figure 6 (SEQ ID NO: 2). The Sac I and Eco RI cloning sites are at positions 6290 and 6314, respectively. Figure 3A also shows M13IX22 where each of the elements necessary for producing a surface expression library between right and left half randomized oligonucleotides is marked.

Library Construction

Each population of right and left half randomized oligonucleotides from columns 1R through 40R and columns 1L through 40L are cloned separately into M13IX42 and M13IX22, respectively, to create sublibraries of right and left half
5 randomized oligonucleotides. Therefore, a total of eighty sublibraries are generated. Separately maintaining each population of randomized oligonucleotides until the final screening step is performed to ensure maximum efficiency of annealing of right and left half oligonucleotides. The
10 greater efficiency increases the total number of randomized oligonucleotides which can be obtained. Alternatively, one can combine all forty populations of right half oligonucleotides (columns 1R-40R) into one population and of left half oligonucleotides (columns 1L-40L) into a
15 second population to generate just one sublibrary for each.

For the generation of sublibraries, each of the above populations of randomized oligonucleotides are cloned separately into the appropriate vector. The right half oligonucleotides are cloned into M13IX42 to generate
20 sublibraries M13IX42.1R through M13IX42.40R. The left half oligonucleotides are similarly cloned into M13IX22 to generate sublibraries M13IX22.1L through M13IX22.40L. Each vector contains unique Eco RI and Sac I restriction enzyme sites which produce 5' and 3' single-stranded overhangs,
25 respectively, when digested. The single strand overhangs are used for the annealing and ligation of the complementary single-stranded random oligonucleotides.

The randomized oligonucleotide populations are cloned between the Eco RI and Sac I sites by sequential
30 digestion and ligation steps. Each vector is treated with an excess of Eco RI (New England Biolabs) at 37°C for 2 hours followed by addition of 4-24 units of calf intestinal alkaline phosphatase (Boehringer Mannheim, Indianapolis, IN). Reactions are stopped by ph nol/chloroform extraction
35 and ethanol precipitation. The pellets are resuspended in

an appropriate amount of distilled or deionized water (dH₂O). About 10 pmol of vector is mixed with a 5000-fold molar excess of each population of randomized oligonucleotides in 10 µl of 1X ligase buffer (50 mM Tris-HCl, pH 7.8, 10 mM MgCl₂, 20 mM DTT, 1 mM ATP, 50 µg/ml BSA) containing 1.0 U of T4 DNA ligase (BRL, Gaithersburg, MD). The ligation is incubated at 16°C for 16 hours. Reactions are stopped by heating at 75°C for 15 minutes and the DNA is digested with an excess of Sac I (New England Biolabs) for 2 hours. Sac I is inactivated by heating at 75°C for 15 minutes and the volume of the reaction mixture is adjusted to 300 µl with an appropriate amount of 10X ligase buffer and dH₂O. One unit of T4 DNA ligase (BRL) is added and the mixture is incubated overnight at 16°C. The DNA is ethanol precipitated and resuspended in TE (10 mM Tris-HCl, pH 8.0, 1 mM EDTA). DNA from each ligation is electroporated into XL1 Blue™ cells (Stratagene, La Jolla, CA), as described below, to generate the sublibraries.

E. coli XL1 Blue™ is electroporated as described by Smith et al., Focus 12:38-40 (1990) which is incorporated herein by reference. The cells are prepared by inoculating a fresh colony of XL1s into 5 mls of SOB without magnesium (20 g bacto-tryptone, 5 g bacto-yeast extract, 0.584 g NaCl, 0.186 g KCl, dH₂O to 1,000 mls) and grown with vigorous aeration overnight at 37°C. SOB without magnesium (500 ml) is inoculated at 1:1000 with the overnight culture and grown with vigorous aeration at 37°C until the OD₅₅₀ is 0.8 (about 2 to 3 h). The cells are harvested by centrifugation at 5,000 rpm (2,600 x g) in a GS3 rotor (Sorvall, Newtown, CT) at 4°C for 10 minutes, resuspended in 500 ml of ice-cold 10% (v/v) sterile glycerol and centrifuged and resuspended a second time in the same manner. After a third centrifugation, the cells are resuspended in 10% sterile glycerol at a final volume of about 2 ml, such that the OD₅₅₀ of the suspension is 200 to 300. Usually, resuspension is achieved in the 10%

glycerol that remains in the bottle after pouring off the supernate. Cells are frozen in 40 μ l aliquots in microcentrifuge tubes using a dry ice-ethanol bath and stored frozen at -70°C .

- 5 Frozen cells are electroporated by thawing slowly on ice before use and mixing with about 10 pg to 500 ng of vector per 40 μ l of cell suspension. A 40 μ l aliquot is placed in an 0.1 cm electroporation chamber (Bio-Rad, Richmond, CA) and pulsed once at 0°C using 200 Ω parallel
10 resistor, 25 μF , 1.88 kV, which gives a pulse length (τ) of ~ 4 ms. A 10 μ l aliquot of the pulsed cells are diluted into 1 ml SOC (98 mls SOB plus 1 ml of 2 M MgCl_2 and 1 ml of 2 M glucose) in a 12- x 75-mm culture tube, and the culture is shaken at 37°C for 1 hour prior to culturing in
15 selective media, (see below).

- Each of the eighty sublibraries are cultured using methods known to one skilled in the art. Such methods can be found in Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold
20 Spring Harbor, 1989, and in Ausubel et al., Current Protocols in Molecular Biology, John Wiley and Sons, New York, 1989, both of which are incorporated herein by reference. Briefly, the above 1 ml sublibrary cultures were grown up by diluting 50-fold into 2XYT media (16 g
25 tryptone, 10 g yeast extract, 5 g NaCl) and culturing at 37°C for 5-8 hours. The bacteria were pelleted by centrifugation at 10,000 xg. The supernatant containing phage was transferred to a sterile tube and stored at 4°C .

- Double strand vector DNA containing right and
30 left half randomized oligonucleotide inserts is isolated from the cell pellet of each sublibrary. Briefly, the pellet is washed in TE (10 mM Tris, pH 8.0, 1 mM EDTA) and recollected by centrifugation at 7,000 rpm for 5' in a Sorval centrifuge (Newtown, CT). Pellets are resuspended

in 6 mls of 10% Sucrose, 50 mM Tris, pH 8.0. 3.0 ml of 10 mg/ μ l lysozyme is added and incubated on ice for 20 minutes. 12 mls of 0.2 M NaOH, 1% SDS is added followed by 10 minutes on ice. The suspensions are then incubated on ice for 20 minutes after addition of 7.5 mls of 3 M NaOAc, pH 4.6. The samples are centrifuged at 15,000 rpm for 15 minutes at 4°C, RNased and extracted with phenol/chloroform, followed by ethanol precipitation. The pellets are resuspended, weighed and an equal weight of CsCl₂ is dissolved into each tube until a density of 1.60 g/ml is achieved. EtBr is added to 600 μ g/ml and the double-stranded DNA is isolated by equilibrium centrifugation in a TV-1665 rotor (Sorval) at 50,000 rpm for 6 hours. These DNAs from each right and left half sublibrary are used to generate forty libraries in which the right and left halves of the randomized oligonucleotides have been randomly joined together.

Each of the forty libraries are produced by joining together one right half and one left half sublibrary. The two sublibraries joined together corresponded to the same column number for right and left half random oligonucleotide synthesis. For example, sublibrary M13IX42.1R is joined with M13IX22.1L to produce the surface expression library M13IX.1RL. In the alternative situation where only two sublibraries are generated from the combined populations of all right half synthesis and all left half synthesis, only one surface expression library would be produced.

For the random joining of each right and left half oligonucleotide populations into a single surface expression vector species, the DNAs isolated from each sublibrary are digested an excess of Fok I (New England Biolabs). The reactions are stopped by phenol/chloroform extraction, followed by ethanol precipitation. Pellets are resuspended in dH₂O. Each surface expression library is

generated by ligating equal molar amounts (5-10 pmol) of Fok I digested DNA isolated from corresponding right and left half sublibraries in 10 μ l of 1X ligase buffer containing 1.0 U of T4 DNA ligase (Bethesda Research Laboratories, Gaithersburg, MD). The ligations proceeded overnight at 16°C and are electroporated into the sup O strain MK30-3 (Boehringer Mannheim Biochemical, (BMB), Indianapolis, IN) as previously described for XL1 cells. Because MK30-3 is sup O, only the vector portions encoding the randomized oligonucleotides which come together will produce viable phage.

Screening of Surface Expression Libraries

Purified phage are prepared from 50 ml liquid cultures of XL1 Blue™ cells (Stratagene) which are infected at a m.o.i. of 10 from the phage stocks stored at 4°C. The cultures are induced with 2 mM IPTG. Supernatants from all cultures are combined and cleared by two centrifugations, and the phage are precipitated by adding 1/7.5 volumes of PEG solution (25% PEG-8000, 2.5 M NaCl), followed by incubation at 4°C overnight. The precipitate is recovered by centrifugation for 90 minutes at 10,000 x g. Phage pellets are resuspended in 25 ml of 0.01 M Tris-HCl, pH 7.6, 1.0 mM EDTA, and 0.1% Sarkosyl and then shaken slowly at room temperature for 30 minutes. The solutions are adjusted to 0.5 M NaCl and to a final concentration of 5% polyethylene glycol. After 2 hours at 4°C, the precipitates containing the phage are recovered by centrifugation for 1 hour at 15,000 X g. The precipitates are resuspended in 10 ml of NET buffer (0.1 M NaCl, 1.0 mM EDTA, and 0.01 M Tris-HCl, pH 7.6), mixed well, and the phage repelleted by centrifugation at 170,000 X g for 3 hours. The phage pellets are subsequently resuspended overnight in 2 ml of NET buffer and subjected to cesium chloride centrifugation for 18 hours at 110,000 X g (3.86 g of cesium chloride in 10 ml of buffer). Phage bands are

collect d, diluted 7-fold with NET buffer, recentrifuged at 170,000 X g for 3 hours, resuspended, and stored at 4°C in 0.3 ml of NET buffer containing 0.1 mM sodium azide.

Ligand binding proteins used for panning on
5 streptavidin coated dishes are first biotinylated and then absorbed against UV-inactivated blocking phage (see below). The biotinylating reagents are dissolved in dimethylformamide at a ratio of 2.4 mg solid NHS-SS-Biotin (sulfosuccinimidyl 2-(biotinamido)ethyl-1,3'-
10 dithiopropionate; Pierce, Rockford, IL) to 1 ml solvent and used as recommended by the manufacturer. Small-scale reactions are accomplished by mixing 1 µl dissolved reagent with 43 µl of 1 mg/ml ligand binding protein diluted in sterile bicarbonate buffer (0.1 M NaHCO₃, pH 8.6). After 2
15 hours at 25°C, residual biotinylating reagent is reacted with 500 µl 1 M ethanolamine (pH adjusted to 9 with HCl) for an additional 2 hours. The entire sample is diluted with 1 ml TBS containing 1 mg/ml BSA, concentrated to about 50 µl on a Centricon 30 ultra-filter (Amicon), and washed
20 on the same filter three times with 2 ml TBS and once with 1 ml TBS containing 0.02% NaN₃ and 7 x 10¹² UV-inactivated blocking phage (see below); the final retentate (60-80 µl) is stored at 4°C. Ligand binding proteins biotinylated with the NHS-SS-Biotin reagent are linked to biotin via a
25 disulfide-containing chain.

UV-irradiated M13 phage were used for blocking binding proteins which fortuitously bound filamentous phage in general. M13mp8 (Messing and Vieira, Gene 19: 262-276 (1982), which is incorporated herein by reference) was
30 chosen because it carries two amber stop codons, which ensure that the few phage surviving irradiation will not grow in the sup O strains used to titer the surface expression libraries. A 5 ml sample containing 5 x 10¹³ M13mp8 phage, purified as described above, was placed in a
35 small petri plate and irradiated with a germicidal lamp at

a distance of two feet for 7 minutes (flux 150 $\mu\text{W}/\text{cm}^2$). NaN_3 was added to 0.02% and phage particles concentrated to 10^{14} particles/ml on a Centricon 30-kDa ultrafilter (Amicon).

5 For panning, polystyrene petri plates (60 x 15 mm, Falcon; Becton Dickinson, Lincoln Park, NJ) are incubated with 1 ml of 1 mg/ml of streptavidin (BMB) in 0.1 M NaHCO_3 , pH 8.6-0.02% NaN_3 in a small, air-tight plastic box overnight in a cold room. The next day streptavidin is
10 removed and replaced with at least 10 ml blocking solution (29 mg/ml of BSA; 3 $\mu\text{g}/\text{ml}$ of streptavidin; 0.1 M NaHCO_3 , pH 8.6-0.02% NaN_3) and incubated at least 1 hour at room temperature. The blocking solution is removed and plates are washed rapidly three times with Tris buffered saline
15 containing 0.5% Tween 20 (TBS-0.5% Tween 20).

Selection of phage expressing peptides bound by the ligand binding proteins is performed with 5 μl (2.7 μg ligand binding protein) of blocked biotinylated ligand binding proteins reacted with a 50 μl portion of each
20 library. Each mixture is incubated overnight at 4°C, diluted with 1 ml TBS-0.5% Tween 20, and transferred to a streptavidin-coated petri plate prepared as described above. After rocking 10 minutes at room temperature, unbound phage are removed and plates washed ten times with
25 TBS-0.5% Tween 20 over a period of 30-90 minutes. Bound phage are eluted from plates with 800 μl sterile elution buffer (1 mg/ml BSA, 0.1 M HCl, pH adjusted to 2.2 with glycerol) for 15 minutes and eluates neutralized with 48 μl 2 M Tris (pH unadjusted). A 20 μl portion of each eluate
30 is titrated on MK30-3 concentrated cells with dilutions of input phage.

A second round of panning is performed by treating 750 μl of first eluate from each library with 5 mM DTT for 10 minutes to break disulfide bonds linking biotin

groups to residual biotinylated binding proteins. The treated eluate is concentrated on a Centricon 30 ultrafilter (Amicon), washed three times with TBS-0.5% Tween 20, and concentrated to a final volume of about 50 μ l. Final retentate is transferred to a tube containing 5.0 μ l (2.7 μ g ligand binding protein) blocked biotinylated ligand binding proteins and incubated overnight. The solution is diluted with 1 ml TBS-0.5% Tween 20, panned, and eluted as described above on fresh streptavidin-coated petri plates. The entire second eluate (800 μ l) is neutralized with 48 μ l 2 M Tris, and 20 μ l is titered simultaneously with the first eluate and dilutions of the input phage.

Individual phage populations are purified through 2 to 3 rounds of plaque purification. Briefly, the second eluate titer plates are lifted with nitrocellulose filters (Schleicher & Schuell, Inc., Keene, NH) and processed by washing for 15 minutes in TBS (10 mM Tris-HCl, pH 7.2, 150 mM NaCl), followed by an incubation with shaking for an additional 1 hour at 37°C with TBS containing 5% nonfat dry milk (TBS-5% NDM) at 0.5 ml/cm². The wash is discarded and fresh TBS-5% NDM is added (0.1 ml/cm²) containing the ligand binding protein between 1 nM to 100 mM, preferably between 1 to 100 μ M. All incubations are carried out in heat-sealable pouches (Sears). Incubation with the ligand binding protein proceeds for 12-16 hours at 4°C with shaking. The filters are removed from the bags and washed 3 times for 30 minutes at room temperature with 150 mls of TBS containing 0.1% NDM and 0.2% NP-40 (Sigma, St. Louis, MO). The filters are then incubated for 2 hours at room temperature in antiserum against the ligand binding protein at an appropriate dilution in TBS-0.5% NDM, washed in 3 changes of TBS containing 0.1% NDM and 0.2% NP-40 as described above and incubated in TBS containing 0.1% NDM and 0.2% NP-40 with 1 x 10⁶ cpm of ¹²⁵I-labeled Protein A (specific activity = 2.1 x 10⁷ cpm/ μ g). After a washing

with TBS containing 0.1% NDM and 0.2% NP-40 as described above, the filters are wrapped in Saran Wrap and exposed to Kodak X-Omat x-ray film (Kodak, Rochester, NY) for 1-12 hours at -70°C using Dupont Cronex Lightning Plus
5 Intensifying Screens (Dupont, Willmington, DE).

Positive plaques identified are cored with the large end of a pasteur pipet and placed into 1 ml of SM (5.8 g NaCl, 2 g $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 50 ml 1 M Tris-HCl, pH 7.5, 5 mls 2% gelatin, to 1000 mls with dH_2O) plus 1-3 drops of
10 CHCl_3 , and incubated at 37°C 2-3 hours or overnight at 4°C. The phage are diluted 1:500 in SM and 2 μl are added to 300 μl of XL1 cells plus 3 mls of soft agar per 100 mm^2 plate. The XL1 cells are prepared for plating by growing a colony overnight in 10 ml LB (10 g bacto-tryptone, 5 g bacto-yeast
15 extract, 10 g NaCl, 1000 ml dH_2O) containing 100 μl of 20% maltose and 100 μl of 1 M MgSO_4 . The bacteria are pelleted by centrifugation at 2000 xg for 10 minutes and the pellet is resuspended gently in 10 mls of 10 mM MgSO_4 . The suspension is diluted 4-fold by adding 30 mls of 10 mM MgSO_4 ,
20 to give an OD_{600} of approximately 0.5. The second and third round screens are identical to that described above except that the plaques are cored with the small end of a pasteur pipet and placed into 0.5 mls SM plus a drop of CHCl_3 , and 1-5 μl of the phage following incubation are used for plating
25 without dilution. At the end of the third round of purification, an individual plaque is picked and the templates prepared for sequencing.

Template Preparation and Sequencing

Templates are prepared for sequencing by
30 inoculating a 1 ml culture of 2XYT containing a 1:100 dilution of an overnight culture of XL1 with an individual plaque. The plaques are picked using a sterile toothpick. The culture is incubated at 37°C for 5-6 hours with shaking and then transferred to a 1.5 ml microfuge tube. 200 μl of

PEG solution is added, followed by vortexing and placed on ice for 10 minutes. The phage precipitate is recovered by centrifugation in a microfuge at 12,000 x g for 5 minutes. The supernatant is discarded and the pellet is resuspended in 230 μ l of TE (10 mM Tris-HCl, pH 7.5, 1 mM EDTA) by gently pipeting with a yellow pipet tip. Phenol (200 μ l) is added, followed by a brief vortex and microfuged to separate the phases. The aqueous phase is transferred to a separate tube and extracted with 200 μ l of phenol/chloroform (1:1) as described above for the phenol extraction. A 0.1 volume of 3 M NaOAc is added, followed by addition of 2.5 volumes of ethanol and precipitated at -20°C for 20 minutes. The precipitated templates are recovered by centrifugation in a microfuge at 12,000 x g for 8 minutes. The pellet is washed in 70% ethanol, dried and resuspended in 25 μ l TE. Sequencing was performed using a Sequenase™ sequencing kit following the protocol supplied by the manufacturer (U.S. Biochemical, Cleveland, OH).

20

EXAMPLE II

Isolation and Characterization of Peptide Ligands Generated From Oligonucleotides Having Random Codons at Two Predetermined Positions

This example shows the generation of a surface expression library from a population of oligonucleotides having randomized codons. The oligonucleotides are n codons in length and are cloned into a single vector species for the generation of a M13 gene VIII-based surface expression library. The example also shows the selection of peptides for a ligand binding protein and characterization of their encoded nucleic acid sequences.

Oligonucleotide Synthesis

Oligonucleotides were synthesized as described in Examp1 I. The synthesizer was programmed to synthesize the sequences shown in Table IX. These sequences correspond to the first random codon position synthesized and 3' flanking sequences of the oligonucleotide which hybridizes to the leader sequence in the vector. The complementary sequences are used for insertional mutagenesis of the synthesized population of oligonucleotides.

10

Table IX

<u>Column</u>	<u>Sequence (5' to 3')</u>
column 1	AA(A/C)GGTTGGTCGGTACCGG
column 2	AG(A/G)GGTTGGTCGGTACCGG
column 3	AT(A/G)GGTTGGTCGGTACCGG
15 column 4	AC(A/G)GGTTGGTCGGTACCGG
column 5	CA(G/T)GGTTGGTCGGTACCGG
column 6	CT(G/C)GGTTGGTCGGTACCGG
column 7	AG(T/C)GGTTGGTCGGTACCGG
column 8	AT(T/C)GGTTGGTCGGTACCGG
20 column 9	CC(A/C)GGTTGGTCGGTACCGG
column 10	T(A/T)TGGTTGGTCGGTACCGG

The next eight random codon positions were synthesized as described for Table V in Example I. Following the ninth position synthesis, the reaction products were once more combined, mixed and redistributed into 10 new reaction columns. Synthesis of the last random codon position and 5' flanking sequences are shown in Table X.

Table X

30

<u>Column</u>	<u>Sequence (5' to 3')</u>
column 1	AGGATCCGCCGAGCTCAA(A/C)A
column 2	AGGATCCGCCGAGCTCAG(A/G)A
column 3	AGGATCCGCCGAGCTCAT(A/G)A

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	column 4	AGGATCCGCCGAGCTCAC(A/G) <u>A</u>
	column 5	AGGATCCGCCGAGCTCCA(G/T) <u>A</u>
	column 6	AGGATCCGCCGAGCTCCT(G/C) <u>A</u>
	column 7	AGGATCCGCCGAGCTCAG(T/C) <u>A</u>
5	column 8	AGGATCCGCCGAGCTCAT(T/C) <u>A</u>
	column 9	AGGATCCGCCGAGCTCCC(A/C) <u>A</u>
	column 10	AGGATCCGCCGAGCTCT(A/T) <u>TA</u>

The reaction products were mixed once more and the oligonucleotides cleaved and purified as recommended by the manufacturer. The purified population of oligonucleotides were used to generate a surface expression library as described below.

Vector Construction

The vector used for generating surface expression libraries from a single oligonucleotide population (i.e., without joining together of right and left half oligonucleotides) is described below. The vector is a M13-based expression vector which directs the synthesis of gene VIII-peptide fusion proteins (Figure 4). This vector exhibits all the functions that the combined right and left half vectors of Example I exhibit.

An M13-based vector was constructed for the cloning and surface expression of populations of random oligonucleotides (Figure 4, M13IX30), M13mpl9 (Pharmacia) was the starting vector. This vector was modified to contain, in addition to the encoded wild type M13 gene VIII: (1) a pseudo-wild type gene, gene VIII sequence with an amber stop codon placed between it and the restriction sites for cloning oligonucleotides; (2) Stu I, Spe I and Xho I restriction sites in frame with the pseudo-wild type gVIII for cloning oligonucleotides; (3) sequences necessary for expression, such as a promoter, signal sequence and translation initiation signals; (4) various other mutations

to remove redundant restriction sites and the amino terminal portion of Lac Z.

Construction of M13IX30 was performed in four steps. In the first step, a precursor vector containing the pseudo gene VIII and various other mutations was constructed, M13IX01F. The second step involved the construction of a small cloning site in a separate M13mp18 vector to yield M13IX03. In the third step, expression sequences and cloning sites were constructed in M13IX03 to generate the intermediate vector M13IX04B. The fourth step involved the incorporation of the newly constructed sequences from the intermediate vector into M13IX01F to yield M13IX30. Incorporation of these sequences linked them with the pseudo gene VIII.

Construction of the precursor vector M13IX01F was similar to that of M13IX42 described in Example I except for the following features: (1) M13mp19 was used as the starting vector; (2) the Fok I site 5' to the unique Eco RI site was not incorporated and the overhang at the naturally occurring Fok I site at position 3547 was not changed to 5'-CTTC-3'; (3) the spacer sequence was not incorporated between the Eco RI and Sac I sites; and (4) the amber codon at position 4492 was not incorporated.

In the second step, M13mp18 was mutated to remove the 5' end of Lac Z up to the Lac i binding site and including the Lac Z ribosome binding site and start codon. Additionally, the polylinker was removed and a Mlu I site was introduced in the coding region of Lac Z. A single oligonucleotide was used for these mutagenesis and had the sequence "5'-AAACGACGCCAGTGCCAAGTGACGCGTGTGAAATTGTTATCC-3'" (SEQ ID NO: 41). Restriction enzymes for Hind III and Eco RI were introduced downstream of the MluI site using the oligonucleotide "5'-GGCGAAAGGGAATTCTGCAAGGCGATTAAGCTTGGGTAACGCC-3'" (SEQ ID NO:

42). These modifications of M13mpl8 yielded the vector M13IX03.

The expression sequences and cloning sites were introduced into M13IX03 by chemically synthesizing a series of oligonucleotides which encode both strands of the
5 desired sequence. The oligonucleotides are presented in Table XI (SEQ ID NOS: 43 through 50).

TABLE XI
M13IX30 Oligonucleotide Series

10	<u>Top Strand</u> <u>Oligonucleotides</u>	<u>Sequence (5' to 3')</u>
	084	GGCGTTACCCAAGCTTTGTACATGGAGAAAATAAAG
	027	TGAAACAAAGCACTATTGCACTGGCACTCTTACCGT TACCGT
15	028	TACTGTTTACCCCTGTGACAAAAGCCGCCAGGTCC AGCTGC
	029	TCGAGTCAGGCCTATTGTGCCCAGGGATTGTACTAG TGGATCCG
20	<u>Bottom</u> <u>Oligonucleotides</u>	<u>Sequence (5' to 3')</u>
	085	TGGCGAAAGGGAATTCGGATCCACTAGTACAATCCCTG
	031	GGCACAATAGGCCTGACTCGAGCAGCTGGACCAGGGCG GCTT
25	032	TTGTCACAGGGGTAAACAGTAACGGTAACGGTAAGTGT GCCA
	033	GTGCAATAGTGCTTTGTTTCACTTTATTTTCTCCATGT ACAA

The above oligonucleotides except for the terminal oligonucleotides 084 (SEQ ID NO: 43) and 085 (SEQ
30 ID NO: 47) of Table XI were mixed, phosphorylated, annealed and ligated to form a double stranded insert as described in Example I. However, instead of cloning directly into

the intermediate vector the insert was first amplified by PCR using the terminal oligonucleotides 084 (SEQ ID NO: 43) and 085 (SEQ ID NO: 47) as primers. The terminal oligonucleotide 084 (SEQ ID NO: 43) contains a Hind III site 10 nucleotides internal to its 5' end. Oligonucleotide 085 (SEQ ID NO: 47) has an Eco RI site at its 5' end. Following amplification, the products were restricted with Hind III and Eco RI and ligated as described in Example I into the polylinker of M13mp18 digested with the same two enzymes. The resultant double stranded insert contained a ribosome binding site, a translation initiation codon followed by a leader sequence and three restriction enzyme sites for cloning random oligonucleotides (Xho I, Stu I, Spe I). The vector was named M13IX04.

During cloning of the double-stranded insert, it was found that one of the GCC codons in oligonucleotides 028 and its complement in 031 was deleted. Since this deletion did not affect function, the final construct is missing one of the two GCC codons. Additionally, oligonucleotide 032 contained a GTG codon where a GAG codon was needed. Mutagenesis was performed using the oligonucleotide 5'-TAACGGTAAGAGTGCCAGTGC-3' (SEQ ID NO: 51) to convert the codon to the desired sequence. The resultant intermediate vector was named M13IX04B.

The fourth step in constructing M13IX30 involved inserting the expression and cloning sequences from M13IX04B upstream of the pseudo-wild type gVIII in M13IX01F. This was accomplished by digesting M13IX04B with Dra III and Ban HI and gel isolating the 700 base pair insert containing the sequences of interest. M13IX01F was likewise digested with Dra III and Bam HI. The insert was combined with the double digested vector at a molar ratio of 3:1 and ligated as described in Example I. It should be noted that all modifications in the vectors described

herein were confirmed by sequence analysis. The sequence of the final construct, M13IX30, is shown in Figure 7 (SEQ ID NO: 3). Figure 4 also shows M13IX30 where each of the elements necessary for surface expression of randomized oligonucleotides is marked.

Library Construction, Screening and Characterization of Encoded Oligonucleotides

Construction of an M13IX30 surface expression library is accomplished identically to that described in Example I for sublibrary construction except the oligonucleotides described above are inserted into M13IX30 by mutagenesis instead of by ligation. The library is constructed and propagated on MK30-3 (BMB) and phage stocks are prepared for infection of XLI cells and screening. The surface expression library is screened and encoding oligonucleotides characterized as described in Example I.

EXAMPLE III

Isolation and Characterization of Peptide Ligands Generated from Right and Left Half Degenerate Oligonucleotides

This example shows the construction and expression of a surface expression library of degenerate oligonucleotides. The encoded peptides of this example derive from the mixing and joining together of two separate oligonucleotide populations. Also demonstrated is the isolation and characterization of peptide ligands and their corresponding nucleotide sequence for specific binding proteins.

Synthesis of Oligonucleotide Populations

A population of left half degenerate

oligonucleotides and a population of right half degenerate oligonucleotides was synthesized using standard automated procedures as described in Example I.

5 The degenerate codon sequences for ach
population of oligonucleotides were generated by
sequentially synthesizing the triplet NNG/T where N is an
equal mixture of all four nucleotides. The antisense
sequence for each population of oligonucleotides was
synthesized and each population contained 5' and 3'
10 flanking sequences complementary to the vector sequence.
The complementary termini was used to incorporate ach
population of oligonucleotides into their respective
vectors by standard mutagenesis procedures. Such
procedures have been described previously in Example I and
15 in the Detailed Description. Synthesis of the antisense
sequence of each population was necessary since the single-
stranded form of the vectors are obtained only as the sense
strand.

 The left half oligonucleotide population was
20 synthesized having the following sequence: 5'-
AGCTCCCGGATGCCTCAGAAGATG(A/CNN),GGCTTTTGCCACAGGGG-3' (SEQ ID
NO: 52). The right half oligonucleotide population was
synthesized having the following sequence: 5'-
CAGCCTCGGATCCGCC(A/CNN),ATG(A/C)GAAT-3' (SEQ ID NO. 53).
25 These two oligonucleotide populations when incorporated
into their respective vectors and joined together encode a
20 codon oligonucleotide having 19 degenerate positions and
an internal predetermined codon sequence.

Vector Construction

30 Modified forms of the previously described
vectors were used for the construction of right and left
half sublibraries. The construction of left half
sublibraries was performed in an M13-based vector termed

M13ED03. This vector is a modified form of the previously described M13IX30 vector and contains all the essential features of both M13IX30 and M13IX22. M13ED03 contains, in addition to a wild type and a pseudo-wild type gene VIII, sequences necessary for expression and two Fok I sites for joining with a right half oligonucleotide sublibrary. Therefore, this vector combines the advantages of both previous vectors in that it can be used for the generation and expression of surface expression libraries from a single oligonucleotide population or it can be joined with a sublibrary to bring together right and left half oligonucleotide populations into a surface expression library.

M13ED03 was constructed in two steps from M13IX30. The first step involved the modification of M13IX30 to remove a redundant sequence and to incorporate a sequence encoding the eight amino-terminal residues of human β -endorphin. The leader sequence was also mutated to increase secretion of the product.

During construction of M13IX04 (an intermediate vector to M13IX30 which is described in Example II), a six nucleotide sequence was duplicated in oligonucleotide 027 (SEQ ID NO: 44) and its complement 032 (SEQ ID NO: 49). This sequence, 5'-TTACCG-3', was deleted by mutagenesis in the construction of M13ED01. The oligonucleotide used for the mutagenesis was 5'-GGTAAACAGTAACGGTAAGAGTGCCAG-3' (SEQ ID NO: 54). The mutation in the leader sequence was generated using the oligonucleotide 5'-GGGCTTTTGCCACAGGGGT-3' (SEQ ID NO: 55). This mutagenesis resulted in the A residue at position 6353 of M13IX30 being changed to a G residue. The resultant vector was designated M13IX32.

To generate M13ED01, the nucleotide sequence encoding β -endorphin (8 amino acid residues of β -endorphin plus 3 extra amino acid residues) was incorporated after

the leader sequence by mutagenesis. The oligonucleotide used had the following sequence: 5'-AGGGTCATCGCCTTCAGCTCCGGATCCCTCAGAAGTCATAAACCCCCCATAGGC TTTTGCCAC-3' (SEQ ID NO: 56). This mutagenesis also
5 removed some of the downstream sequences through the Spe I site.

The second step in the construction of M13ED03 involved vector changes which put the β -endorphin sequence in frame with the downstream pseudo-gene VIII sequence and
10 incorporated a Fok I site for joining with a sublibrary of right half oligonucleotides. This vector was designed to incorporate oligonucleotide populations by mutagenesis using sequences complementary to those flanking or overlapping with the encoded β -endorphin sequence. The
15 absence of β -endorphin expression after mutagenesis can therefore be used to measure the mutagenesis frequency. In addition to the above vector changes, M13ED03 was also modified to contain an amber codon at position 3262 for biological selection during joining of right and left half
20 sublibraries.

The mutations were incorporated using standard mutagenesis procedures as described in Example I. The frame shift changes and Fok I site were generated using the
o l i g o n u c l e o t i d e 5 ' -
25 TCGCCTTCAGCTCCCGGATGCCTCAGAAGCATGAACCCCCCATAGGC-3' (SEQ ID NO: 57). The amber codon was generated using the oligonucleotide 5'-CAATTTTATCCTAAATCTTACCAAC-3' (SEQ ID NO: 58). The full sequence of the resultant vector, M13ED03, is provided in Figure 8 (SEQ ID NO: 4).

30 The construction of right half oligonucleotide sublibraries was performed in a modified form of the M13IX42 vector. The new vector, M13IX421, is identical to M13IX42 except that the amber codon between the Eco RI-SacI cloning site and the pseudo-gene VIII sequence was removed.

This change ensures that all expression off of the Lac Z promoter produces a peptide-gene VIII fusion protein. Removal of the amber codon was performed by mutagenesis using the following oligonucleotide: 5'-
5 GCCTTCAGCCTCGGATCCGCC-3' (SEQ ID NO: 59). The full sequence of M13IX421 is shown in Figure 9 (SEQ ID NO: 5).

Library Construction, Screening and Characterization of Encoded Oligonucleotides

A sublibrary was constructed for each of the
10 previously described degenerate populations of oligonucleotides. The left half population of oligonucleotides was incorporated into M13ED03 to generate the sublibrary M13ED03.L and the right half population of oligonucleotides was incorporated into M13IX421 to generate
15 the sublibrary M13IX421.R. Each of the oligonucleotide populations were incorporated into their respective vectors using site-directed mutagenesis as described in Example I. Briefly, the nucleotide sequences flanking the degenerate codon sequences were complementary to the vector at the
20 site of incorporation. The populations of nucleotides were hybridized to single-stranded M13ED03 or M13IX421 vectors and extended with T4 DNA polymerase to generate a double-stranded circular vector. Mutant templates were obtained by uridine selection in vivo, as described by Kunkel et
25 al., supra. Each of the vector populations were electroporated into host cells and propagated as described in Example I.

The random joining of right and left half sublibraries into a single surface expression library was
30 accomplished as described in Example I except that prior to digesting each vector population with Fok I they were first digested with an enzyme that cuts in the unwanted portion of each vector. Briefly, M13ED03.L was digested with Bgl II (cuts at 7094) and M13IX421.R was digested with Hind III

(cuts at 3919). Each of the digested populations were further treated with alkaline phosphatase to ensure that the ends would not religate and then digested with an excess of Fok I. Ligations, electroporation and
5 propagation of the resultant library was performed as described in Example I.

The surface expression library was screened for ligand binding proteins using a modified panning procedure.
10 Briefly, 1 ml of the library, about 10^{12} phage particles, was added to 1-5 μ g of the ligand binding protein. The ligand binding protein was either an antibody or receptor globulin (Rg) molecule, Aruffo et al., Cell 61:1303-1313 (1990), which is incorporated herein by reference. Phage
15 were incubated shaking with affinity ligand at room temperature for 1 to 3 hours followed by the addition of 200 μ l of 1 μ m latex beads (Biosite, San Diego, CA) which were coated with goat-antimouse IgG. This mixture was incubated shaking for an additional 1-2 hours at room
20 temperature. Beads were pelleted for 2 minutes by centrifugation in a microfuge and washed with TBS which can contain 0.1% Tween 20. Three additional washes were performed where the last wash did not contain any Tween 20.

Beads containing bound phage were added to plates at
25 a concentration that produces a suitable density for plaque identification screening and sequencing of positive clones (i.e., plated at confluency for rare clones and 200-500 plaques/plate if pure plaques were needed). Briefly, plaques grown for about 6 hours at 37°C were overlaid with
30 nitrocellulose filters that had been soaked in 2 mM IPTG and briefly dried. The filters remained on the plaques overnight at room temperature, removed and placed in blocking solution for 1-2 hours. Following blocking, the filters were incubated in 1 μ g/ml ligand binding protein in
35 blocking solution for 1-2 hours at room temperature. Goat antimouse Ig-coupled alkaline phosphatase (Fisher) was

added at a 1:1000 dilution and the filters were rapidly washed with 10 mls of TBS or block solution over a glass vacuum filter. Positive plaques were identified after alkaline phosphatase development for detection.

- 5 Alternatively, the bound phage were eluted from the beads using 200 μ l 0.1 M Glycine-HCl, pH 2.2, for 15 minutes and the beads were removed by centrifugation. The supernatant containing phage (eluate) was removed and phage exhibiting binding to the ligand binding protein were
10 further enriched by one to two more cycles of panning. The eluates were screened by plaque formation, as described above. Typical yields after the first eluate were about 1×10^6 - 5×10^6 pfu. The second and third eluate generally yielded about 5×10^6 - 2×10^7 pfu and 5×10^7 - 1×10^{10}
15 pfu, respectively.

- Screening of the degenerate oligonucleotide library with several different ligand binding proteins resulted in the identification of peptide sequences which bound to each of the ligands. For example, screening with
20 an antibody to β -endorphin resulted in the detection of about 30-40 different clones which essentially all had the core amino acid sequence known to interact with the antibody. The sequences flanking the core sequences were different showing that they were independently derived and
25 not duplicates of the same clone. Screening with an antibody known as 57 gave similar results (i.e., a core consensus sequence was identified but the flanking sequences among the clones were different).

EXAMPLE IV

30 Generation of a Left Half Random Oligonucleotide Library

This example shows the synthesis and construction of a left half random oligonucleotide library.

A population of random oligonucleotides nine codons in length was synthesized as described in Example I except that different sequences at their 5' and 3' ends were synthesized so that they could be easily inserted into the vector by mutagenesis. Also, the mixing and dividing steps for generating random distributions of reaction products was performed by the alternative method of dispensing equal volumes of bead suspensions. The liquid chosen that was dense enough for the beads to remain dispersed was 100% acetonitrile.

Briefly, each column was prepared for the first coupling reaction by suspending 22 mg (1 μ mole) of 48 μ mol/g capacity beads (Genta, San Diego, CA) in 0.5 mls of 100% acetonitrile. These beads are smaller than those described in Example I and are derivatized with a guanine nucleotide. They also do not have a controlled pore size. The bead suspension was then transferred to an empty reaction column. Suspensions were kept relatively dispersed by gently pipetting the suspension during transfer. Columns were plugged and monomer coupling reactions were performed as shown in Table XII.

Table XII

	<u>Column</u>	<u>Sequence</u> <u>(5' to 3')</u>
25	column 1L	AA(A/C)GGCTTTTGCCACAGG
	column 2L	AG(A/G)GGCTTTTGCCACAGG
	column 3L	AT(A/G)GGCTTTTGCCACAGG
	column 4L	AC(A/G)GGCTTTTGCCACAGG
	column 5L	CA(G/T)GGCTTTTGCCACAGG
30	column 6L	CT(G/C)GGCTTTTGCCACAGG
	column 7L	AG(T/C)GGCTTTTGCCACAGG
	column 8L	AT(T/C)GGCTTTTGCCACAGG
	column 9L	CC(A/C)GGCTTTTGCCACAGG
	column 10L	T(A/T)TGGCTTTTGCCACAGG

After coupling of the last monomer, the columns were unplugged as described previously and their contents were poured into a 1.5 ml microfuge tube. The columns were rinsed with 100% acetonitrile to recover any remaining beads. The volume used for rinsing was determined so that the final volume of total bead suspension was about 100 μ l for each new reaction column that the beads would be aliquoted into. The mixture was vortexed gently to produce a uniformly dispersed suspension and then divided, with constant pipetting of the mixture, into equal volumes. Each mixture of beads was then transferred to an empty reaction column. The empty tubes were washed with a small volume of 100% acetonitrile and also transferred to their respective columns. Random codon positions 2 through 9 were then synthesized as described in Example I where the mixing and dividing steps were performed using a suspension in 100% acetonitrile. The coupling reactions for codon positions 2 through 9 are shown in Table XIII.

Table XIII

20	<u>Column</u>	<u>Sequence</u> <u>(5' to 3')</u>
	column 1L	AA(A/C)A
	column 2L	AG(A/G)A
	column 3L	AT(A/G)A
25	column 4L	AC(A/G)A
	column 5L	CA(G/T)A
	column 6L	CT(G/C)A
	column 7L	AG(T/C)A
	column 8L	AT(T/C)A
30	column 9L	CC(A/C)A
	column 10L	T(A/T)TA

After coupling of the last monomer for the ninth codon position, the reaction products were mixed and a portion was transferred to an empty reaction column.

Columns were plugged and the following monomer coupling reactions were performed: 5'-CGGATGCCTCAGAAGCCCCXXA-3' (SEQ ID NO: 60). The resulting population of random oligonucleotides was purified and incorporated by
5 mutagenesis into the left half vector M13ED04.

M13ED04 is a modified version of the M13ED03 vector described in Example III and therefore contains all the features of that vector. The difference between M13ED03 and M13ED04 is that M13ED04 does not contain the
10 five amino acid sequence (Tyr Gly Gly Phe Met) recognized by anti- β -endorphin antibody. This sequence was deleted by mutagenesis using the oligonucleotide 5'-CGGATGCCTCAGAAGGGCTTTTGCCACAGG (SEQ ID NO: 61). The entire
nucleotide sequence of this vector is shown in Figure 10
15 (SEQ ID NO: 6).

EXAMPLE V

Generation of Soluble, Conformationally-Constrained Random Peptides

This example shows the synthesis and construction
20 of expressible oligonucleotides encoding soluble peptides having a constrained secondary structure in solution.

As noted previously, the binding affinity of a peptide for a ligand-binding protein is a function of the primary and secondary structure of the peptide. The effect
25 of primary structure on affinity may be determined as disclosed in the above examples.

In its broadest form, the disclosed method provides oligonucleotides that are synthesized having a desired bias of predetermined codons such that the
30 oligonucleotides encode peptides having a constrained secondary structure in aqueous solution. In a preferred

mbodiment, oligonucleotides encoding peptides having a constrained secondary structure are synthesized having a desired bias of predetermined codons such that the predetermined codons are separated by at least one random
5 codon.

Oligonucleotides having more than one tuplet encoding an amino acid capable of forming a covalent bond at a predetermined position and the remaining positions having random tuplets are synthesized using the methods
10 described herein. The synthesis steps are similar to those outlined above using twenty or less reaction vessels except that prior to synthesis of the specified codon position, the dividing of the supports into separate reaction vessels for synthesis of different codons is omitted. For example,
15 if the codon at the second position of the oligonucleotide is to be specified, then following synthesis of random codons at the first position and mixing of the supports, the mixed supports are not divided into new reaction vessels but, instead, are contained in a single reaction
20 vessel to synthesize the specified codon. The specified codon is synthesized sequentially from individual monomers as described above. Thus, the number of reaction vessels is increased or decreased at each step to allow for the synthesis of a specified codon or a desired number of
25 random codons.

Alternatively, a population of random left and right precursor oligonucleotides are synthesized essentially as described in Example I, except that at least one predetermined codon encoding cysteine, lysine, glutamic
30 acid, leucine or tyrosine is incorporated into each oligonucleotide. Combination of right and left oligonucleotides results in a single oligonucleotide containing at least two predetermined codons. Alternatively, a population of random oligonucleotides is
35 synthesized as described in Example II, except that at

least two predetermined codons encoding cysteine, lysine, glutamic acid, leucine or tyrosine are incorporated into only one of the two precursor oligonucleotide populations.

Following expression of the oligonucleotides, a peptide having a constrained secondary structure is obtained by allowing the formation of at least one intra-peptide covalent bond. One skilled in the art would know the conditions necessary to allow formation of the particular covalent bond. See, for example, Proteins, Structures and Molecular Principles, Creighton, T.E. ed., W.H. Freeman and Co., New York (1984), incorporated herein by reference. Although oligonucleotides can encode peptides capable of forming more than one intra-peptide covalent bond, only one such bond is necessary to form a conformationally-constrained peptide.

The peptide libraries are expressed on the surface of a cell, for example, a bacteriophage. Phage expressing peptide ligands are initially identified by panning, essentially as described in Example I, except that the phage are first incubated in the presence of a ligand-binding protein (in this example, an antibody), then panned in protein A-coated dishes. Individual phage populations are purified through three rounds of plaque purification, essentially as described in Example I.

Two phage encoding peptides showing significantly higher ligand binding affinity than the general phage population are isolated, the oligonucleotide sequences are determined and the amino acid sequences deduced. The ligand binds with highest affinity to a twenty-two amino acid peptide having the sequence TQSKCSTDHWLG YIEYFIMCTY (SEQ. ID. NO.: 62). The ligand also binds with high affinity to a peptide having the sequence CDDQYYTDHEQ GKCEVALYYTG (SEQ. ID. NO.: 63).

The above-identified peptides are each capable of forming several intra-peptide covalent bonds. For example, a disulfide bond may form between two cysteine residues, a $\epsilon(\gamma\text{-glutamyl})\text{-lysine}$ bond may form between lysine and glutamic acid residues, a lysinonorleucine bond may form between lysine and leucine residues or a dityrosine bond can form between two tyrosine residues (Devlin, Textbook of Biochemistry 3d ed. (1992)). In addition, other peptides can be constructed that contain, for example, four lysine residues, which can form the heterocyclic structure of desmosine.

The nature of the covalent bond in the peptide having the sequence TQSKCSTDHWLGYIEYFIMCTY (SEQ. ID. NO.: 62) is determined by examining the effect of amino acid substitutions on the binding affinity of the ligand, by methods known to those skilled in the art, and described herein. Creighton, *supra*, pp. 335-396, incorporated herein by reference.

The oligonucleotide encoding this peptide is cloned into a vector that allowed secretion of the expressed peptide. The peptide TQSKCSTDHWLGYIEYFIMCTY (SEQ. ID. NO.: 62) is soluble at a concentration of 4 mg/ml. The same peptide, except containing the substitution of alanine for cysteine is insoluble at this concentration.

EXAMPLE VI

Binding Studies Using Conformationally Constrained Peptides

The association constant (K_a), dissociation constant (K_d) and affinity constant (K) were determined for the reaction of a monoclonal antibody with the linear or the cyclized form of a peptide, using a BIAcore automated biosensor (Pharmacia Biosensor AB, Uppsala, Sweden), as

d scribed by Karlsson et al., J. Immunol. Meth. 145:229-240 (1991). A 24 amino acid peptide, TQSKCSTDHWLGYIEYFIMCTYRR (SEQ. ID. NO.: 64), which is recognized by the J2B9 monoclonal antibody, was used for these experiments. The
5 peptide contains two cysteine residues that form a disulfide bond under oxidizing conditions.

The cyclized form of the peptide was immobilized by its amino terminus to the BIAcore sensor chip and exposed to 0.016, 0.033, 0.066, 0.13 or 2.3 nM solutions of
10 the J2B9 antibody. Changes in refractive index were measured and the formulas described by Karlsson et al., supra, were used to calculate the following rate and affinity constants: $K_a = 3.7 \times 10^5 \text{ M}^{-1}\text{s}^{-1}$; $K_d = 4.5 \times 10^{-4} \text{ sec}^{-1}$ and $K = 8.4 \times 10^8 \text{ M}$.

15 After the above-described measurements were obtained, the disulfide bond was reduced by treating the cyclized peptide with 10 mM dithiothreitol, while the peptide was still attached to the BIAcore sensor chip. The dissociation rate of the linear peptide and the J2B9
20 monoclonal antibody was then determined, as described above.

The dissociation rate of the J2B9 antibody and the linear peptide was calculated to be $1.54 \times 10^{-3} \text{ sec}$. Thus, the antibody dissociated from the linear peptide
25 three times faster than it dissociated from the cyclized peptide. Reoxidation of the linearized peptide to reform the cyclized peptide resulted in the dissociation rate again decreasing to the 10^{-4} range. These results show that a conformationally constrained peptide binds a specific
30 receptor with greater affinity than a peptide with a less stable secondary structure.

EXAMPLE VIISoluble, Conformationally-Constrained Random Peptides
Having High Affinity to An Anti-Tetanus Toxin Antibody

5 This example shows the synthesis and construction of
expressible random oligonucleotides encoding soluble
peptides with constrained secondary structures and the
selection of high affinity binders to an anti-tetanus
toxin antibody.

Oligonucleotide Synthesis

10 Random oligonucleotides of ten codons in length were
synthesized as right and left half precursors essentially
as described in Example I. When combined, they yield an
oligonucleotide coding for twenty amino acid long random
peptides. Codons for cysteine were used to produce
15 peptides with a potential for forming covalent bonds for
secondary structure constraints. In contrast to that
described in Example V where the amino acids used for
cyclization of the peptides were placed at predetermined
positions, the cysteine codons were introduced at all
20 positions with a predetermined bias compared to the other
nineteen random codons.

Briefly, ten reaction vessels were used for the
synthesis of twenty random codons at each codon position
essentially as described in Example I. In addition to
25 the normal ten reaction vessels used for synthesis, an
extra two reaction vessels were used for the synthesis of
the two cysteine codons, TGC and TGT. Thus, the
synthesis procedure used a total of twelve reaction
vessels for the synthesis of each codon position where
30 the frequency of cysteine codons at each position is
twenty percent. The 5' and 3' flanking sequences for the
right and left half oligonucleotides were those described

in Example I. The use of the extra two vessels encoding cysteine residues results in the increased frequency of cysteine being incorporated at each codon position. This increased frequency insures the presence of residues
5 capable of forming covalent bonds for constraining the peptide's secondary structure. Moreover, the random incorporation of cysteines at each of the codon positions, instead of incorporation at predetermined positions, increases the probability of obtaining
10 peptides with a constrained conformation and, thus, a high affinity toward a binding protein since a greater number of peptides are available to screen.

Library Construction and Screening

Library construction from right and left half
15 oligonucleotides were generated as described in Example I. The libraries were screened for peptides that bind to an anti-tetanus toxin antibody essentially as described in Example III. After two rounds of panning, eight phage clones were selected that showed high affinity binding to
20 the antibody. Sequencing of the encoding nucleic acids revealed seven peptides having cysteines spaced at ten residues apart and one peptide having cysteines were seven residues apart. The sequences are shown in Table XIV and are listed in the sequencing listing as SEQ ID
25 NOS: 65 through 72.

Table XIV

Conformationally Constrained Peptides Having High
Affinity for Anti-Tetanus Toxin Antibody

	<u>SEQ ID NO:</u>	<u>PEPTIDE SEQUENCE</u>
5	65	TCLREEFILQCYIVMIEDWY
	66	ICEHHQMLLQCSLVCEECEMM
	67	KCIIGWYTLTCYMSDRPRME
	68	ACTQDMNWITCPMYCEVLCF
	69	VCFYFPFKMMCHMEYIAYEY
10	70	DANCGHCTYMCICKIMYYIS
	71	WHRHVSSPMSCWWYDQCAVA
	72	CVQIDFFTVQCNISSHMFLP

Although the invention has been described with reference to the presently preferred embodiment, it should be understood that various modifications can be made without departing from the spirit of the invention. Accordingly, the invention is limited only by the claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: IXSYS, INC.
- (ii) TITLE OF INVENTION: Soluble Peptides Having Constrained, Secondary Conformation in Solution and Method of Making Same.
- (iii) NUMBER OF SEQUENCES: 72
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Campbell and Flores
 - (B) STREET: 4370 La Jolla Village Drive, Suite 700
 - (C) CITY: San Diego
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 92122
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 10-NOV-1993
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/978,893
 - (B) FILING DATE: 10-NOV-1992
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Konski, Antoinette F.
 - (B) REGISTRATION NUMBER: 34,202
 - (C) REFERENCE/DOCKET NUMBER: FP-IX 9769
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (619) 535-9001
 - (E) TELEFAX: (619) 535-8949

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: circular

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AATGCTACTA CTATTAGTAG AATTGATGCC ACCTTTTCAG CTCGCGCCCC AAATGAAAAT	60
ATAGCTAAAC AGGTTATTGA CCATTTGCGA AATGTATCTA ATGGTCAAAC TAAATCTACT	120
CGTTCGCAGA ATTGGGAATC AACTGTTACA TGAATGAAA CTTCCAGACA CCGTACTTTA	180
GTTGCATATT TAAAACATGT TGAGCTACAG CACCAGATTC AGCAATTAAG CTCTAAGCCA	240
TCTGCAAAAA TGACCTCTTA TCAAAAGGAG CAATTAAAGG TACTCTCTAA TCCTGACCTG	300

TTGGAGTTTG	CTTCCGGTCT	GGTTCGCTTT	GAAGCTCGAA	TTAAAACGCG	ATATTTGAAG	360
TCTTTTCGGGC	TTCTCTTAA	TCTTTTGTAT	GCAATCCGCT	TTGCTTCTGA	CTATAATAGT	420
CAGGGTAAAG	ACCTGATTTT	TGATTTATGG	TCATTCTCGT	TTTCTGAACT	GTTTAAAGCA	480
TTTGAGGGGG	ATTCAATGAA	TATTTATGAC	GATTCCGCAG	TATTGGACGC	TATCCAGTCT	540
AAACATTTTA	CTATTACCCC	CTCTGGCAAA	ACTTCTTTTG	CAAAAGCCTC	TCGCTATTTT	600
GGTTTTTATC	GTCGTCTGGT	AAACGAGGGT	TATGATAGTG	TTGCTCTTAC	TATGCCTCGT	660
AATTCCTTTT	GGCGTTATGT	ATCTGCATTA	GTTGAATGTG	GTATTCCTAA	ATCTCAACTG	720
ATGAATCTTT	CTACCTGTAA	TAATGTTGTT	CCGTTAGTTC	GTTTTATTAA	CGTAGATTTT	780
TCTTCCCAAC	GTCCTGACTG	GTATAATGAG	CCAGTTCTTA	AAATCGCATA	AGGTAATTCA	840
CAATGATTAA	AGTTGAAATT	AAACCATCTC	AAGCCCAATT	TACTACTCGT	TCTGGTGTTT	900
CTCGTCAGGG	CAAGCCTTAT	TCACTGAATG	AGCAGCTTTG	TTACGTTGAT	TTGGGTAATG	960
AATATCCGGT	TCTTGTCAAG	ATTACTCTTG	ATGAAGGTCA	GCCAGCCTAT	GCGCCTGGTC	1020
TGTACACCGT	TCATCTGTCC	TCTTTCAAAG	TTGGTCAGTT	CGGTTCCCTT	ATGATTGACC	1080
GTCTGCGCCT	CGTTCCGGCT	AAGTAACATG	GAGCAGGTCG	CGGATTTCTGA	CACAATTTAT	1140
CAGGCGATGA	TACAAATCTC	CGTTGTACTT	TGTTTCGCGC	TTGGTATAAT	CGCTGGGGGT	1200
CAAAGATGAG	TGTTTTAGTG	TATTCTTTTCG	CCTCTTTTCGT	TTTAGGTTGG	TGCCTTCGTA	1260
GTGGCATTAC	GTATTTTACC	CGTTTAATGG	AAACTTCCTC	ATGAAAAAGT	CTTTAGTCCT	1320
CAAAGCCTCT	GTAGCCGTTG	CTACCCTCGT	TCCGATGCTG	TCTTTCGCTG	CTGAGGGTGA	1380
CGATCCCGCA	AAAGCGGCCT	TTAACTCCCT	GCAAGCCTCA	GCGACCGAAT	ATATCGGTTA	1440
TGCGTGCGCG	ATGGTTGTTG	TCATTGTCCG	CGCAACTATC	GGTATCAAGC	TGTTTAAGAA	1500
ATTCACCTCG	AAAGCAAGCT	GATAAACCGA	TACAATTAAA	GGCTCCTTTT	GGAGCCTTTT	1560
TTTTTGGAGA	TTTTCAACGT	GAAAAAATTA	TTATTCGCAA	TTCTTTTAGT	TGTTCCTTTC	1620
TATTCTCACT	CCGCTGAAAC	TGTTGAAAGT	TGTTTAGCAA	AACCCCATAC	AGAAAATTCA	1680
TTTACTAACG	TCTGGAAAGA	CGACAAACT	TTAGATCGTT	ACGCTAATA	TGAGGGTTGT	1740
CTGTGGAATG	CTACAGGCGT	TGTAGTTTGT	ACTGGTGACG	AAACTCAGTG	TTACGGTACA	1800
TGGGTTCCTA	TTGGGCTTGC	TATCCCTGAA	AATGAGGGTG	GTGGCTCTGA	GGGTGGCGGT	1860
TCTGAGGGTG	GCGGTTCTGA	GGGTGGCGGT	ACTAAACCTC	CTGAGTACGG	TGATACACCT	1920
ATTCGGGGCT	ATACTTATAT	CAACCCTCTC	GACGGCACTT	ATCCGCCTGG	TACTGAGCAA	1980
AACCCCGCTA	ATCCTAATCC	TTCTCTTGAG	GAGTCTCAGC	CTCTTAATAC	TTTCATGTTT	2040
CAGAATAATA	GGTTCCGAAA	TAGGCAGGGG	GCATTAATCTG	TTTATACGGG	CACTGTTACT	2100
CAAGGCACTG	ACCCCGTTAA	AACTTATTAC	CAGTACACTC	CTGTATCATC	AAAAGCCATG	2160
TATGACGCTT	ACTGGAACGG	TAAATTCAGA	GACTGCGCTT	TCCATTCTGG	CTTTAATGAA	2220
GATCCATTCTG	TTTGTGAATA	TCAAGGCCAA	TCGTCTGACC	TGCCTCAACC	TCCTGTCAAT	2280
GCTGGCGGCG	GCTCTGGTGG	TGTTCTGGT	GCGGCTCTG	AGGGTGGTGG	CTCTGAGGGT	2340

GGCGGTTCTG	AGGGTGGCGG	CTCTGAGGGA	GGCGGTTCCG	GTGGTGGCTC	TGGTTCCGGT	2400
GATTTTGATT	ATGAAAAGAT	GGCAAACGCT	AATAAGGGGG	CTATGACCGA	AAATGCCGAT	2460
GAAAACGCGC	TACAGTCTGA	CGCTAAAGGC	AAACTTGATT	CTGTCGCTAC	TGATTACGGT	2520
GCTGCTATCG	ATGGTTTCAT	TGGTGACGTT	TCCGGCCTTG	CTAATGGTAA	TGGTGCTACT	2580
GGTGATTTTG	CTGGCTCTAA	TTCCCAAATG	GCTCAAGTCG	GTGACGGTGA	TAATTCACCT	2640
TTAATGAATA	ATTTCCGTCA	ATATTTACCT	TCCCTCCCTC	AATCGGTTGA	ATGTCGCCCT	2700
TTTGTCTTTA	GCGCTGGTAA	ACCATATGAA	TTTCTATTG	ATTGTGACAA	AATAAACTTA	2760
TTCCGTGGTG	TCTTTGCGTT	TCTTTTATAT	GTTGCCACCT	TTATGTATGT	ATTTTCTACG	2820
TTTGCTAACA	TACTGCGTAA	TAAGGAGTCT	TAATCATGCC	AGTTCTTTTG	GGTATTCCGT	2880
TATTATTGCG	TTTCCTCGGT	TTCTTCTG	TAACTTTGTT	CGGCTATCTG	CTTACTTTTC	2940
TTAAAAAGGG	CTTCGGTAAG	ATAGCTATTG	CTATTTCAAT	GTTTCTTGCT	CTTATTATTG	3000
GGCTTAACTC	AATTCCTGTG	GGTATCTCT	CTGATATTAG	CGCTCAATTA	CCCTCTGACT	3060
TTGTTCAGGG	TGTTCAAGTA	ATTCTCCCGT	CTAATGCGCT	TCCCTGTTTT	TATGTTATTC	3120
TCTCTGTAAA	GGCTGCTATT	TTCATTTTTG	ACGTTAAACA	AAAAATCGTT	TCTTATTTGG	3180
ATTGGGATAA	ATAATATGGC	TGTTTATTTT	GTAACGGCA	AATTAGGCTC	TGGAAAGACG	3240
CTCGTTAGCG	TTGGTAAGAT	TCAGGATAAA	ATTGTAGCTG	GGTGCAAAAT	AGCAACTAAT	3300
CTTGATTTAA	GGCTTCAAAA	CCTCCCGCAA	GTCGGGAGGT	TCGCTAAAC	GCCTCGCGTT	3360
CTTAGAATAC	CGGATAAGCC	TTCTATATCT	GATTTGCTTG	CTATTGGGCG	CGGTAATGAT	3420
TCCTACGATG	AAAATAAAAA	CGGCTTGCTT	GTTCTCGATG	AGTGCGGTAC	TTGGTTTAAT	3480
ACCCGTTCTT	GGAATGATAA	GGAAAGACAG	CCGATTATTG	ATTGGTTTCT	ACATGCTCGT	3540
AAATTAGGAT	GGGATATTAT	CTTCCTTGTT	CAGGACTTAT	CTATTGTTGA	TAAACAGGCG	3600
CGTTCTGCAT	TAGCTGAACA	TGTTGTTTAT	TGTCGTCGTC	TGGACAGAAT	TACTTTACCT	3660
TTTGTGCGTA	CTTTATATTC	TCTTATTACT	GGCTCGAAAA	TGCCTCTGCC	TAAATTACAT	3720
GTTGGCGTTG	TTAAATATGG	CGATTCTCAA	TTAAGCCCTA	CTGTTGAGCG	TTGGCTTTAT	3780
ACTGGTAAGA	ATTTGTATAA	CGCATATGAT	ACTAAACAGG	CTTTTTCTAG	TAATTATGAT	3840
TCCGGTGTTT	ATTCTTATTT	AACGCCTTAT	TTATCACACG	GTCGGTATTT	CAAACCATTA	3900
AATTTAGGTC	AGAAGATGAA	GCTTACTAAA	ATATATTTGA	AAAAGTTTTT	ACGCGTTCTT	3960
TGTCTTGCGA	TTGGATTGTC	ATCAGCATTT	ACATATAGTT	ATATAACCCA	ACCTAAGCCG	4020
GAGGTAAAAA	AGGTAGTCTC	TCAGACCTAT	GATTTTGATA	AATTCACAT	TGACTCTTCT	4080
CAGCGTCTTA	ATCTAAGCTA	TCGCTATGTT	TTCAAGGATT	CTAAGGGAAA	ATTAATTAAT	4140
AGCGACGATT	TACAGAAGCA	AGGTTATTCA	CTCACATATA	TTGATTTATG	TACTGTTTCC	4200
ATTAAAAAGG	TAATTCAAAT	GAAATTGTTA	AATGTAATTA	ATTTTGTTTT	CTTGATGTTT	4260
GTTTCATCAT	CTTCTTTTGC	TCAGGTAATT	GAAATGAATA	ATTCGCCTCT	GCGCGATTTT	4320
GTAACCTGGT	ATTCAAAAGCA	ATCAGGCGAA	TCCGTTATTG	TTTCTCCCGA	TGTAAAAGGT	4380

ACTGTTACTG	TATATTCATC	TGACGTTAAA	CCTGAAAATC	TACGCAATTT	CTTTATTTCT	4440
GTTTTACGTG	CTAATAATTT	TGATATGGTT	GGTTCAATTC	CTTCCATTAT	TTAGAAGTAT	4500
AATCCAAACA	ATCAGGATTA	TATTGATGAA	TTGCCATCAT	CTGATAATCA	GGAATATGAT	4560
GATAATTCGG	CTCCTTCTGG	TGGTTTCTTT	GTTCCGCAAA	ATGATAATGT	TACTCAAAC	4620
TTTAAAATTA	ATAACGTTTC	GGCAAAGGAT	TTAATACGAG	TTGTCGAATT	GTTTGTAAG	4680
TCTAATACTT	CTAAATCCTC	AAATGTATTA	TCTATTGACG	GCTCTAATCT	ATTAGTTGTT	4740
AGTGACCTA	AAGATATTTT	AGATAACCTT	CCTCAATTCC	TTTCTACTGT	TGATTTGCCA	4800
ACTGACCAGA	TATTGATTGA	GGGTTTGATA	TTTGAGGTC	AGCAAGGTGA	TGCTTTAGAT	4860
TTTTCATTTG	CTGCTGGCTC	TCAGCGTGGC	ACTGTTGCAG	GCGGTGTAA	TACTGACCGC	4920
CTCACCTCTG	TTTTATCTTC	TGCTGGTGGT	TCGTTGCGTA	TTTTTAATGG	CGATGTTTTA	4980
GGGCTATCAG	TTCGCGCATT	AAAGACTAAT	AGCCATTCAA	AAATATTGTC	TGTGCCACGT	5040
ATTCTTACGC	TTTCAGGTCA	GAAGGGTTCT	ATCTCTGTTG	GCCAGAATGT	CCCTTTTATT	5100
ACTGGTCGTG	TGACTGGTGA	ATCTGCCAAT	GTAAATAATC	CATTTGAGAC	GATTGAGCGT	5160
CAAATGTAG	GTATTTCCAT	GAGCGTTTTT	CCTGTTGCAA	TGGCTGGCGG	TAATATTGTT	5220
CTGGATATTA	CCAGCAAGGC	CGATAGTTTG	AGTTCTTCTA	CTCAGGCAAG	TGATGTTATT	5280
ACTAATCAAA	GAAGTATTGC	TACAACGGTT	AATTTGCGTG	ATGGACAGAC	TCTTTTACTC	5340
GGTGGCCTCA	CTGATTATAA	AAACACTTCT	CAAGATTCTG	GCGTACCGTT	CCTGTCTAAA	5400
ATCCCTTTAA	TCGGCCTCCT	GTTTAGCTCC	CGCTCTGATT	CCAACGAGGA	AAGCACGTTA	5460
TACGTGCTCG	TCAAAGCAAC	CATAGTACGC	GCCCTGTAGC	GGCGCATTAA	GCGCGGCGGG	5520
TGTGGTGGTT	ACGCGCAGCG	TGACCGCTAC	ACTTGCCAGC	GCCCTAGCGC	CCGCTCCTTT	5580
CGCTTTCTTC	CCTTCCTTTC	TCGCCACGTT	CGCCGGCTTT	CCCCGTCAAG	CTCTAAATCG	5640
GGGGCTCCCT	TTAGGGTTCC	GATTTAGTGC	TTTACGGCAC	CTCGACCCCA	AAAACTTGA	5700
TTTGGGTGAT	GGTTCACGTA	GTGGGCCATC	GCCCTGATAG	ACGGTTTTTC	GCCCTTTGAC	5760
GTTGGAGTCC	ACGTTCTTTA	ATAGTGGACT	CTTGTTCCAA	ACTGGAACAA	CACTCAACCC	5820
TATCTCGGGC	TATTCTTTTG	ATTATAAGG	GATTTTGCCG	ATTCGGAAC	CACCATCAAA	5880
CAGGATTTTC	GCCTGCTGGG	GCAAACCAGC	GTGGACCGCT	TGCTGCAACT	CTCTCAGGGC	5940
CAGGCGGTGA	AGGGCAATCA	GCTGTTGCCC	GTCTCGCTGG	TGAAAAGAAA	AACCACCCTG	6000
GCGCCCAATA	CGCAAACCGC	CTCTCCCCGC	GCGTTGGCCG	ATTCATTAAT	GCAGCTGGCA	6060
CGACAGGTTT	CCCAGCTGGA	AAGCGGGCAG	TGAGCGCAAC	GCAATTAATG	TGAGTTAGCT	6120
CACTCATTAG	GCACCCCAGG	CTTTACACTT	TATGCTTCCG	GCTCGTATGT	TGTGTGGAAT	6180
TGTGAGCGGA	TAACAATTTT	ACACAGGAAA	CAGCTATGAC	CAGGATGTAC	GAATTCGCAG	6240
GTAGGAGAGC	TCGGCGGATC	CTAGGCTGAA	GGCGATGACC	CTGCTAAGGC	TGCATTCAAT	6300
AGTTTACAGG	CAAGTGCTAC	TGAGTACATT	GGCTACGCTT	GGGCTATGGT	AGTAGTTATA	6360
GTTGGTGCTA	CCATAGGGAT	TAAATTATTC	AAAAAGTTTA	CGAGCAAGGC	TTCTTAACCA	6420

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GCTGGCGTAA	TAGCGAAGAG	GCCCCGACCG	ATCGCCCTTC	CCAACAGTTG	CGCAGCCTGA	6480
ATGGCGAATG	GCGCTTTGCC	TGGTTTCCGG	CACCAGAAGC	GGTGCCGGAA	AGCTGGCTGG	6540
AGTGCGATCT	TCCTGAGGCC	GATACGGTCG	TCGTCCCCCTC	AAACTGGCAG	ATGCACGGTT	6600
ACGATGCGCC	CATCTACACC	AACGTAACT	ATCCCATTAC	GGTCAATCCG	CCGTTTGTTT	6660
CCACGGAGAA	TCCGACGGGT	TGTTACTCGC	TCACATTTAA	TGTTGATGAA	AGCTGGCTAC	6720
AGGAAGGCCA	GACGCGAATT	ATTTTTGATG	GCGTTCCTAT	TGGTTAAAAA	ATGAGCTGAT	6780
TTAACAAAAA	TTTAACGCGA	ATTTTAACAA	AATATTAACG	TTTACAATTT	AAATATTTGC	6840
TTATACAATC	TTCTGTGTTT	TGGGGCTTTT	CTGATTATCA	ACCGGGGTAC	ATATGATTGA	6900
CATGCTAGTT	TTACGATTAC	CGTTCATCGA	TTCTCTTGTT	TGCTCCAGAC	TCTCAGGCAA	6960
TGACCTGATA	GCCTTTGTAG	ATCTCTCAAA	AATAGCTACC	CTCTCCGGCA	TTAATTTATC	7020
AGCTAGAACG	GTTGAATATC	ATATTGATGG	TGATTTGACT	GTCTCCGGCC	TTTCTCACCC	7080
TTTTGAATCT	TTACCTACAC	ATTACTCAGG	CATTGCATTT	AAAATATATG	AGGGTCTTAA	7140
AAATTTTTAT	CCTTGCGTTG	AAATAAAGGC	TTCTCCCGCA	AAAGTATTAC	AGGGTCATAA	7200
TGTTTTTGGT	ACAACCGATT	TAGCTTTATG	CTCTGAGGCT	TTATTGCTTA	ATTTTGCTAA	7260
TTCTTTGCCT	TGCCTGTATG	ATTTATTGGA	CGTT			7294

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: circular

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AATGCTACTA	CTATTAGTAG	AATTGATGCC	ACCTTTTCAG	CTCGCGCCCC	AAATGAAAAT	60
ATAGCTAAAC	AGGTTATTGA	CCATTGCGA	AATGTATCTA	ATGGTCAAAC	TAAATCTACT	120
CGTTTCGAGA	ATTGGGAATC	AACTGTTACA	TGGAATGAAA	CTTCCAGACA	CCGTACTTTA	180
GTTGCATATT	TAAAACATGT	TGAGCTACAG	CACCAGATTC	AGCAATTAAG	CTCTAAGCCA	240
TCTGCAAAAA	TGACCTCTTA	TCAAAAGGAG	CAATTAAAGG	TACTCTCTAA	TCCTGACCTG	300
TTGGAGTTTG	CTTCCGGTCT	GGTTCGCTTT	GAAGCTCGAA	TTAAAACGCG	ATATTTGAAG	360
TCTTTTCGGG	TTCTCTTAA	TCTTTTTGAT	GCAATCCGCT	TTGCTTCTGA	CTATAATAGT	420
CAGGGTAAAG	ACCTGATTTT	TGATTTATGG	TCATTCTCGT	TTTCTGAACT	GTTTAAAGCA	480
TTTGAGGGGG	ATTCAATGAA	TATTTATGAC	GATTCCGCAG	TATGGACGC	TATCCAGTCT	540
AAACATTTTA	CTATTACCCC	CTCTGGCAAA	ACTTCTTTTG	CAAAGCCTC	TCGCTATTTT	600
GGTTTTTATC	GTCGTCTGGT	AAACGAGGGT	TATGATAGTG	TTGCTCTTAC	TATGCCTCGT	660
AATTCCTTTT	GGCGTTATGT	ATCTGCATTA	GTTGAATGTG	GTATTCCTAA	ATCTCAACTG	720
ATGAATCTTT	CTACCTGTAA	TAATGTTGTT	CCGTTAGTTC	GTTTTATTAA	CGTAGATTTT	780

TCTTCCCAAC	GTCCTGACTG	GTATAATGAG	CCAGTTCTTA	AAATCGCATA	AGGTAATTCA	840
CAATGATTAA	AGTTGAAATT	AAACCATCTC	AAGCCCAATT	TACTACTCGT	TCTGGTGTTT	900
CTCGTCAGGG	CAAGCCTTAT	TCACTGAATG	AGCAGCTTTG	TTACGTTGAT	TTGGGTAATG	960
AATATCCGGT	TCTTGTCAAG	ATTACTCTTG	ATGAAGGTCA	GCCAGCCTAT	GCGCCTGGTC	1020
TGTACACCGT	TCATCTGTCC	TCTTTCAAAG	TTGGTCAGTT	CGGTTCCCTT	ATGATTGACC	1080
GTCTGCGCCT	CGTTCCGGCT	AAGTAACATG	GAGCAGGTGCG	CGGATTTCTGA	CACAATTTAT	1140
CAGGCGATGA	TACAAATCTC	CGTTGTACTT	TGTTTCGCGC	TTGGTATAAT	CGCTGGGGGT	1200
CAAAGATGAG	TGTTTTAGTG	TATTCCTTCG	CCTCTTTCGT	TTTAGGTTGG	TGCCTTCGTA	1260
GTGGCATTAC	GTATTTTACC	CGTTTAATGG	AAACTTCCTC	ATGAAAAAGT	CTTTAGTCCCT	1320
CAAAGCCTCT	GTAGCCGTTG	CTACCCTCGT	TCCGATGCTG	TCTTTCGCTG	CTGAGGGTGA	1380
CGATCCCGCA	AAAGCGGCCT	TTAACTCCCT	GCAAGCCTCA	GCGACCGAAT	ATATCGGTGA	1440
TGCGTGGGCG	ATGGTTGTTG	TCATTGTCGG	CGCAACTATC	GGTATCAAGC	TGTTTAAGAA	1500
ATTCACCTCG	AAAGCAAGCT	GATAAACCGA	TACAATTAAA	GGCTCCTTTT	GGAGCCTTTT	1560
TTTTTGAGAG	TTTTCAACGT	GAAAAAATTA	TTATTCGCAA	TTCTTTTAGT	TGTTCCCTTC	1620
TATTCTCACT	CCGCTGAAAC	TGTTGAAAGT	TGTTTAGCAA	AACCCCATAC	AGAAAATTCA	1680
TTTACTAACG	TCTGGAAAGA	CGACAAAAC	TTAGATCGTT	ACGCTAACTA	TGAGGGTTGT	1740
CTGTGGAATG	CTACAGGCGT	TGTAGTTTGT	ACTGGTGACG	AAACTCAGTG	TTACGGTACA	1800
TGGGTTCCCTA	TTGGGCTTGC	TATCCCTGAA	AATGAGGGTG	GTGGCTCTGA	GGGTGGCGGT	1860
TCTGAGGGTG	GCGGTTCTGA	GGGTGGCGGT	ACTAAACCTC	CTGAGTACGG	TGATACACCT	1920
ATTCCGGGCT	ATACTTATAT	CAACCCTCTC	GACGGCACTT	ATCCGCCTGG	TACTGAGCAA	1980
AACCCCGCTA	ATCCTAATCC	TTCTCTTGAG	GAGTCTCAGC	CTCTTAATAC	TTTCATGTTT	2040
CAGAATAATA	GGTTCCGAAA	TAGGCAGGGG	GCATTAACTG	TTTATACGGG	CACTGTTACT	2100
CAAGGCACTG	ACCCCGTTAA	AACTTATTAC	CAGTACACTC	CTGTATCATC	AAAAGCCATG	2160
TATGACGCTT	ACTGGAACGG	TAAATTCAGA	GACTGCGCTT	TCCATTCTGG	CTTTAATGAA	2220
GATCCATTCTG	TTTGTGAATA	TCAAGGCCAA	TCGTCTGACC	TGCCTCAACC	TCCTGTCAAT	2280
GCTGGCGGCG	GCTCTGGTGG	TGGTCTGGT	GGCGGCTCTG	AGGGTGGTGG	CTCTGAGGGT	2340
GGCGGTTCTG	AGGGTGGCGG	CTCTGAGGGA	GGCGGTTCCG	GTGGTGGCTC	TGGTCCGGT	2400
GATTTTGATT	ATGAAAAGAT	GGCAAACGCT	AATAAGGGGG	CTATGACCGA	AAATGCCGAT	2460
GAAAACGCGC	TACAGTCTGA	CGCTAAAGGC	AAACTTGATT	CTGTCGCTAC	TGATTACGGT	2520
GCTGCTATCG	ATGGTTTCAT	TGGTGACGTT	TCCGGCCTTG	CTAATGGTAA	TGGTGCTACT	2580
GGTGATTTTG	CTGGCTCTAA	TTCCCAAATG	GCTCAAGTCG	GTGACGGTGA	TAATTCACCT	2640
TTAATGAATA	ATTTCCTGCA	ATATTTACCT	TCCCTCCCTC	AATCGGTTGA	ATGTCGCCCT	2700
TTTGTCTTTA	GCGCTGGTAA	ACCATATGAA	TTTTCTATTG	ATTGTGACAA	AATAAACTTA	2760
TTCCGTGGTG	TCTTTGCGTT	TCTTTTATAT	GTTGCCACCT	TTATGTATGT	ATTTTCTACG	2820

TTTGCTAACA	TACTGCGTAA	TAAGGAGTCT	TAATCATGCC	AGTTCTTTTG	GGTATTCCGT	2880
TATTATTGCG	TTTCCTCGGT	TTCCTTCTGG	TAACCTTGTT	CGGCTATCTG	CTTACTTTTC	2940
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GGCTTAACTC	AATTCTTGTTG	GGTTATCTCT	CTGATATTAG	CGCTCAATTA	CCCTCTGACT	3060
TTGTTTCAGGG	TGTTTCAGTTA	ATTCTCCCGT	CTAATGCGCT	TCCCTGTTTT	TATGTTATTC	3120
TCTCTGTAAA	GGCTGCTATT	TTCATTTTTG	ACGTAAACA	AAAAATCGTT	TCTTATTTGG	3180
ATTGGGATAA	ATAATATGGC	TGTTTATTTT	GTAAGTGGCA	AATTAGGCTC	TGGAAAGACG	3240
CTCGTTAGCG	TTGGTAAGAT	TAGGATAAAA	ATTGTAGCTG	GGTGCAAAAT	AGCAACTAAT	3300
CTTGATTTAA	GGCTTCAAAA	CCTCCCGCAA	GTCGGGAGGT	TCGCTAAAC	GCCTCGCGTT	3360
CTTAGAATAC	CGGATAAGCC	TTCTATATCT	GATTTGCTTG	CTATTGGGCG	CGGTAATGAT	3420
TCCTACGATG	AAAATAAAAA	CGGCTTGCTT	GTTCTCGATG	AGTGCGGTAC	TTGGTTTAAT	3480
ACCCGTTCTT	GGAATGATAA	GGAAAGACAG	CCGATTATTG	ATTGGTTTCT	ACATGCTCGT	3540
AAATTAGGAT	GGGATATTAT	CTTCCTTGTT	CAGGACTTAT	CTATTGTTGA	TAAACAGGCG	3600
CGTTCTGCAT	TAGCTGAACA	TGTTGTTTAT	TGTCGTCGTC	TGGACAGAAT	TACTTTACCT	3660
TTTGTCGGTA	CTTTATATTC	TCTTATTACT	GGCTCGAAAA	TGCCTCTGCC	TAAATTACAT	3720
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ACTGGTAAGA	ATTTGTATAA	CGCATATGAT	ACTAAACAGG	CTTTTTCTAG	TAATTATGAT	3840
TCCGGTGTTT	ATTCTTATTT	AACGCCCTAT	TTATCACACG	GTCGGTATTT	CAAACCATT	3900
AATTTAGGTC	AGAAGATGAA	ATTAACATAA	ATATATTGTA	AAAAGTTTTT	TCGCGTTCTT	3960
TGTCTTGCGA	TTGGATTTGC	ATCAGCATTT	ACATATAGTT	ATATAACCCA	ACCTAAGCCG	4020
GAGGTAAAAA	AGGTAGTCTC	TCAGACCTAT	GATTTTGATA	AATTCATAT	TGACTCTTCT	4080
CAGCGTCTTA	ATCTAAGCTA	TCGCTATGTT	TTCAAGGATT	CTAAGGGAAA	ATTAATTAAT	4140
AGCGACGATT	TACAGAAGCA	AGGTTATTCA	CTCACATATA	TTGATTTATG	TACTGTTTCC	4200
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TGTTTCATCA	TCTTCTTTTG	CTCAGGTAAT	TGAAATGAAT	AATTCGCCTC	TGCGCGATTT	4320
TGTAACCTGG	TATTCAAAGC	AATCAGGCGA	ATCCGTTATT	GTTTCTCCCG	ATGTAAAGG	4380
TACTGTTACT	GTATATTCAT	CTGACGTTAA	ACCTGAAAAT	CTACGCAATT	TCTTTATTTT	4440
TGTTTTACGT	GCTAATAATT	TTGATATGGT	TSGTTCAATT	CCTTCATAA	TTCAGAAGTA	4500
TAATCCAAAC	AATCAGGATT	ATATTGATGA	ATTGCCATCA	TCTGATAATC	AGGAATATGA	4560
TGATAATTCC	GCTCCTTCTG	GTGGTTTCTT	TGTTCCGCAA	AATGATAATG	TTACTCAAAC	4620
TTTTAAATTT	AATAACGTTT	GGGCAAAGGA	TTAATACGA	GTTGTCGAAT	TGTTTGTAAG	4680
GTCTAATACT	TCTAAATCC	CAAATGTATT	ATCTATTGAC	GGCTCTAATC	TATTAGTTGT	4740
TAGTGCACCT	AAAGATATTT	TAGATAACCT	TCCTCAATTC	CTTTCTACTG	TTGATTTGCC	4800
AACTGACCAG	ATATTGATTG	AGGGTTTGAT	ATTTGAGGTT	CAGCAAGGTG	ATGCTTTAGA	4860

TTTTTCATTT	GCTGCTGGCT	CTCAGCGTGG	CACTGTTGCA	GGCGGTGTTA	ATACTGACCG	4920
CCTCACCTCT	GTTTTATCTT	CTGCTGGTGG	TTCGTTCCGT	ATTTTAAATG	GCGATGTTTT	4980
AGGGCTATCA	GTTCGCGCAT	TAAAGACTAA	TAGCCATTCA	AAAATATTGT	CTGTGCCACG	5040
TATTCTTACG	CTTTCAGGTC	AGAAGGGTTC	TATCTCTGTT	GGCCAGAATG	TCCCTTTTAT	5100
TACTGGTCGT	GTGACTGGTG	AATCTGCCAA	TGTAAATAAT	CCATTTTCAGA	CGATTGAGCG	5160
TCAAAATGTA	GGTATTTCCA	TGAGCGTTTT	TCCTGTTGCA	ATGGCTGGCG	GTAATATTGT	5220
TCTGGATATT	ACCAGCAAGG	CCGATAGTTT	GAGTTCCTCT	ACTCAGGCAA	GTGATGTTAT	5280
TACTAATCAA	AGAAGTATTG	CTACAACGGT	TAATTTGCGT	GATGGACAGA	CTCTTTTACT	5340
CGGTGGCCTC	ACTGATTATA	AAAACACTTC	TCAAGATTCT	GGCGTACCGT	TCCTGTCTAA	5400
AATCCCTTTA	ATCGGCCTCC	TGTTTAGCTC	CCGCTCTGAT	TCCAACGAGG	AAAGCACGTT	5460
ATACGTGCTC	GTCAAAGCAA	CCATAGTACG	CGCCCTGTAG	CGGCGCATT	AGCGCGGCGG	5520
GTGTGGTGGT	TACGCGCAGC	GTGACCGCTA	CACTTGCCAG	CGCCCTAGCG	CCCCTCCTT	5580
TCGCTTTCTT	CCCTTCCTTT	CTCGCCACGT	TCGCCGGCTT	TCCCCGTCAA	GCTCTAAATC	5640
GGGGGCTCCC	TTAGGGTTC	CGATTTAGTG	CTTTACGGCA	CCTCGACCCC	AAAAAAGTTG	5700
ATTTGGGTGA	TGGTTCACGT	AGTGGGCCAT	CGCCCTGATA	GACGGTTTTT	CGCCCTTTGA	5760
CGTTGGAGTC	CACGTTCTTT	AATAGTGGAC	TCTTGTTCCA	AACTGGAACA	ACACTCAACC	5820
CTATCTCGGG	CTATTCTTTT	GATTTATAAG	GGATTTTGCC	GATTTTCGGAA	CCACCATCAA	5880
ACAGGATTTT	CGCCTGCTGG	GGCAAACCAG	CGTGGACCGC	TTGCTGCAAC	TCTCTCAGGG	5940
CCAGGCGGTG	AAGGGCAATC	AGCTGTTGCC	CGTCTCGCTG	GTGAAAAGAA	AAACCACCTT	6000
GGCGCCCAAT	ACGCAAACCG	CCTCTCCCCG	CGCGTTGGCC	GATTCATTAA	TGCAGCTGGC	6060
ACGACAGGTT	TCCCGACTGG	AAAGCGGGCA	GTGAGCGCAA	CGCAATTAAT	GTGAGTTAGC	6120
TCACTCATT	GGCACCCAG	GCTTTACACT	TTATGCTTCC	GGCTCGTATG	TTGTGTGGAA	6180
TTGTGAGCGG	ATAACAATTT	CACACGCCAA	GGAGACAGTC	ATAATGAAAT	ACCTATTGCC	6240
TACGGCAGCC	GCTGGATTGT	TATTACTCGC	TGCCCAACCA	GCCATGGCCG	AGCTCGTGAT	6300
GACCCAGACT	CCAGAATTCC	ATCCGGAATG	AGTGTTAATT	CTAGAACGCG	TAAGCTTGGC	6360
ACTGGCCGTC	GTTTACAAAC	GTCGTGACTG	GGAAAACCTT	GGCGTTACCC	AACTTAATCG	6420
CCTTGCAGCA	CACCCCCCTT	TCGCCAGCTG	GCGTAATAGC	GAAGAGGCCC	GCACCGATCG	6480
CCCTTCCCAA	CAGTTGCGCA	GCCTGAATGG	CGAATGGCGC	TTTGCTGGT	TTCCGGCACC	6540
AGAAGCGGTG	CCGAAAGCT	GGCTGGAGTG	CGATCTTCCT	GAGGCCGATA	CGGTCTGTCG	6600
CCCCTCAAAC	TGGCAGATGC	ACGGTTACGA	TGCGCCCATC	TACACCAACG	TAACCTATCC	6660
CATTACGGTC	AATCCGCCGT	TTGTTCCAC	GGAGAATCCG	ACGGGTTGTT	ACTCGCTCAC	6720
ATTTAATGTT	GATGAAAGCT	GGCTACAGGA	AGGCCAGACG	CGAATTATTT	TTGATGGCGT	6780
TCCTATTGGT	TAAAAAATGA	GCTGATTTAA	CAAAAATTTA	ACGCGAATTT	TAACAAAATA	6840
TTAACGTTTA	CAATTTAAAT	ATTTGCTTAT	ACAATCTTCC	TGTTTTTGGG	GCTTTTCTGA	6900

TTATCAACCG	GGGTACATAT	GATTGACATG	CTAGTTTAC	GATTACCGTT	CATCGATTCT	6960
CTTGTTTGCT	CCAGACTCTC	AGGCAATGAC	CTGATAGCCT	TTGTAGATCT	CTCAAAAATA	7020
GCTACCCTCT	CCGGCATTAA	TTTATCAGCT	AGAACGGTTG	AATATCATAT	TGATGGTGAT	7080
TTGACTGTCT	CCGGCCTTTC	TCACCCTTTT	GAATCTTTAC	CTACACATTA	CTCAGGCATT	7140
GCATTTAAAA	TATATGAGGG	TTCTAAAAAT	TTTTATCCTT	GCGTTGAAAT	AAAGGCTTCT	7200
CCCGCAAAAG	TATTACAGGG	TCATAATGTT	TTTGGTACAA	CCGATTTAGC	TTTATGCTCT	7260
GAGGCTTTAT	TGCTTAATTT	TGCTAATTCT	TTGCCTTGCC	TGTATGATTT	ATTGGACGTT	7320

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: circular

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AATGCTACTA	CTATTAGTAG	AATTGATGCC	ACCTTTTCAG	CTCGCGCCCC	AAATGAAAAT	60
ATAGCTAAAC	AGGTTATTGA	CCATTTGCGA	AATGTATCTA	ATGGTCAAAC	TAAATCTACT	120
CGTTCGCAGA	ATTGGGAATC	AACTGTTACA	TGGAATGAAA	CTTCCAGACA	CCGTACTTTA	180
GTTGCATATT	TAAAACATGT	TGAGCTACAG	CACCAGATTC	AGCAATTAAG	CTCTAAGCCA	240
TCTGCAAAAA	TGACCTCTTA	TCAAAAGGAG	CAATTAAAGG	TACTCTCTAA	TCCTGACCTG	300
TTGGAGTTTG	CTTCCGGTCT	GGTTCGCTTT	GAAGCTCGAA	TTAAAACGCG	ATATTTGAAG	360
TCTTTCGGGC	TTCCTCTTAA	TCTTTTTGAT	GCAATCCGCT	TTGCTTCTGA	CTATAATAGT	420
CAGGGTAAAG	ACCTGATTTT	TGATTTATGG	TCATTCTCGT	TTTCTGAACT	GTTTAAAGCA	480
TTTGAGGGGG	ATTCAATGAA	TATTTATGAC	GATTCCGCAG	TATTGGACGC	TATCCAGTCT	540
AAACATTTTA	CTATTACCCC	CTCTGGCAAA	ACTTCTTTTG	CAAAGCCTC	TCGCTATTTT	600
GGTTTTTATC	GTCGTCTGGT	AAACGAGGGT	TATGATAGTG	TTGCTCTTAC	TATGCCTCGT	660
AATTCCTTTT	GGCGTTATGT	ATCTGCATTA	GTTGAATGTG	GTATTCCTAA	ATCTCAACTG	720
ATGAATCTTT	CTACCTGTAA	TAATGTTGTT	CCGTTAGTTC	GTTTTATTAA	CGTAGATTTT	780
TCTTCCCAAC	GTCCTGACTG	GTATAATGAG	CCAGTTCTTA	AAATCGCATA	AGGTAATTCA	840
CAATGATTAA	AGTTGAAATT	AAACCATCTC	AAGCCCAATT	TACTACTCGT	TCTGGTGTTT	900
CTCGTCAGGG	CAAGCCTTAT	TCACTGAATG	AGCAGCTTTG	TTACGTTGAT	TTGGGTAATG	960
AATATCCGGT	TCTTGTC AAG	ATTACTCTTG	ATGAAGGTCA	GCCAGCCTAT	GCGCCTGGTC	1020
TGTACACCGT	TCATCTGTCC	TCTTTCAAAG	TTGGTCAGTT	CGGTTCCCTT	ATGATTGACC	1080
GTCTGCGCCT	CGTTCCGGCT	AAGTAACATG	GAGCAGGTG	CGGATTTCGA	CACAATTTAT	1140
CAGGCGATGA	TACAAATCTC	CGTTGTACTT	TGTTTCGCGC	TTGGTATAAT	CGCTGGGGGT	1200

CAAAGATGAG	TGTTTTAGTG	TATTCTTTTCG	CCTCTTTTCGT	TTTAGGTTGG	TGCCTTCGTA	1260
GTGGCATTAC	GTATTTTACC	CGTTTAAATGG	AAACTTCCTC	ATGAAAAAGT	CTTTAGTCCT	1320
CAAAGCCTCT	GTAGCCGTTG	CTACCCTCGT	TCCGATGCTG	TCTTTCGCTG	CTGAGGGTGA	1380
CGATCCCGCA	AAAGCGGCCT	TTAACTCCCT	GCAAGCCTCA	GCGACCGAAT	ATATCGGTTA	1440
TGCGTGCGG	ATGGTTGTTG	TCATTGTCCG	CGCAACTATC	GSTATCAAGC	TGTTTAAGAA	1500
ATTCACCTCG	AAAGCAAGCT	GATAAACCGA	TACAATTAAA	GGCTCCTTTT	GGAGCCTTTT	1560
TTTTTGGAGA	TTTTCAACGT	AAAAAAATTA	TTATTCGCAA	TTCCTTTAGT	TGTTCTTTTC	1620
TATTCTCACT	CCGCTGAAAC	TGTTGAAAGT	TGTTTAGCAA	AACCCCATAC	AGAAAATTCA	1680
TTTACTAACG	TCTGGAAAGA	CGACAAAAC	TTAGATCGTT	ACGCTAACTA	TGAGGGTTGT	1740
CTGTGGAATG	CTACAGGCGT	TGTAGTTTGT	ACTGGTGACG	AAACTCAGTG	TTACGGTACA	1800
TGGGTTCCTA	TTGGGCTTGC	TATCCCTGAA	AATGAGGGTG	GTGGCTCTGA	GGGTGGCGGT	1860
TCTGAGGGTG	GCGGTTCTGA	GGGTGGCGGT	ACTAAACCTC	CTGAGTACGG	TGATACACCT	1920
ATTCCGGGCT	ATACTTATAT	CAACCCTCTC	GACGGCACTT	ATCCGCCTGG	TACTGAGCAA	1980
AACCCCGCTA	ATCCTAATCC	TTCTCTTGAG	GAGTCTCAGC	CTCTTAATAC	TTTCATGTTT	2040
CAGAATAATA	GGTTCCGAAA	TAGGCAGGGG	GCATTAAGTG	TTTATACGGG	CACTGTTACT	2100
CAAGGCACTG	ACCCCGTTAA	AACCTATTAC	CAGTACACTC	CTGTATCATC	AAAAGCCATG	2160
TATGACGCTT	ACTGGAACGG	TAAATTCAGA	GACTGCGCTT	TCCATTCTGG	CTTTAATGAA	2220
GATCCATTCTG	TTTGTGAATA	TCAAGGCCAA	TCGTCTGACC	TGCCTCAACC	TCCTGTCAAT	2280
GCTGGCGGCG	GCTCTGGTGG	TGGTTCTGGT	GGCGGCTCTG	AGGGTGGTGG	CTCTGAGGGT	2340
GGCGGTTCTG	AGGGTGGCGG	CTCTGAGGGA	GGCGGTTCCG	GTGGTGGCTC	TGGTTCCGGT	2400
GATTTTGATT	ATGAAAAGAT	GGCAAACGCT	AATAAGGGGG	CTATGACCGA	AAATGCCGAT	2460
GAAAACGCGC	TACAGTCTGA	CGCTAAAGGC	AAACTTGATT	CTGTCGCTAC	TGATTACGGT	2520
GCTGCTATCG	ATGGTTTCAT	TGGTGACGTT	TCCGGCCTTG	CTAATGGTAA	TGGTGCTACT	2580
GGTGATTTTG	CTGGCTCTAA	TTCCCAAATG	GCTCAAGTCG	GTGACGGTGA	TAATTCACCT	2640
TTAATGAATA	ATTTCCGTCA	ATATTTACCT	TCCCTCCCTC	AATCGGTTGA	ATGTCGCCCT	2700
TTTGTCTTTA	GCGCTGGTAA	ACCATATGAA	TTTTCTATTG	ATTGTGACAA	AATAAACTTA	2760
TTCCGTGGTG	TCTTTGCGTT	TCTTTTATAT	GTTGCCACCT	TTATGTATGT	ATTTTCTACG	2820
TTTGCTAACA	TACTGCGTAA	TAAGGAGTCT	TAATCATGCC	AGTTCTTTTG	GGTATTCCGT	2880
TATTATTGCG	TTTCCTCGGT	TTCCTTCTGG	TAACTTGTG	CGGCTATCTG	CTTACTTTTC	2940
TTAAAAAGGG	CTTCGGTAAG	ATAGCTATTG	CTATTTTCATT	GTTTCTTGCT	CTTATTATTG	3000
GGCTTAACTC	AATTCTTGTTG	GGTTATCTCT	CTGATATTAG	CGCTCAATTA	CCCTCTGACT	3060
TTGTTCAAGG	TGTTCAAGTTA	ATTCTCCCGT	CTAATGCGCT	TCCCTGTTTT	TATGTTATTC	3120
TCTCTGTAAA	GGCTGCTATT	TTCATTTTTG	ACGTAAACA	AAAAATCGTT	TCTTATTTGG	3180
ATTGGGATAA	ATAATATGGC	TGTTTATTTT	GTAAGTGGCA	AATTAGGCTC	TGGAAAGACG	3240

CTCGTTAGCG	TTGGTAAGAT	TCAGGATAAA	ATTGTAGCTG	GGTGCAAAAT	AGCAACTAAT	3300
CTTGATTTAA	GGCTTCAAAA	CCTCCCGCAA	GTCGGGAGGT	TCGCTAAAC	GCCTCGCGTT	3360
CTTAGAATAC	CGGATAAGCC	TTCTATATCT	GATTTGCTTG	CTATTGGGCG	CGGTAATGAT	3420
TCCTACGATG	AAAATAAAAA	CGGCTTGCTT	GTTCTCGATG	AGTGCGGTAC	TTGGTTTAAT	3480
ACCCGTTCTT	GGAATGATAA	GGAAAGACAG	CCGATTATTG	ATTGGTTTCT	ACATGCTCGT	3540
AAATTAGGAT	GGGATATTAT	TTTTCTTGTT	CAGGACTTAT	CTATTGTTGA	TAAACAGGCG	3600
CGTTCTGCAT	TAGCTGAACA	TGTTGTTTAT	TGTCGTCGTC	TGGACAGAAT	TACTTTACCT	3660
TTTGTCGGTA	CTTTATATTC	TCTTATTACT	GGCTCGAAAA	TGCCTCTGCC	TAAATTACAT	3720
GTTGGCGTTG	TTAAATATGG	CGATTCTCAA	TTAAGCCCTA	CTGTTGAGCG	TTGGCTTTAT	3780
ACTGGTAAGA	ATTTGTATAA	CGCATATGAT	ACTAAACAGG	CTTTTCTAG	TAATTATGAT	3840
TCCGGTGTTT	ATTCTTATTT	AACGCCTTAT	TTATCACACG	GTCGGTATTT	CAAACCATTA	3900
AATTTAGGTC	AGAAGATGAA	GCTTACTAAA	ATATATTTGA	AAAAGTTTTT	ACGCGTTCTT	3960
TGTCTTGCGA	TTGGATTTGC	ATCAGCATTT	ACATATAGTT	ATATAACCCA	ACCTAAGCCG	4020
GAGGTAAAA	AGGTAGTCTC	TCAGACCTAT	GATTTTGATA	AATTCACAT	TGACTCTTCT	4080
CAGCGTCTTA	ATCTAAGCTA	TCGCTATGTT	TTCAAGGATT	CTAAGGGAAA	ATTAATTAAT	4140
AGCGACGATT	TACAGAAGCA	AGGTATTCA	CTCACATATA	TTGATTTATG	TACTGTTTCC	4200
ATTAAAAAAG	GTAATTCAAA	TGAAATTGTT	AAATGTAATT	AATTTTGTTT	TCTTGATGTT	4260
TGTTTCATCA	TCTTCTTTTG	CTCAGGTAAT	TGAAATGAAT	AATTCGCCTC	TGCGCGATTT	4320
TGTAACCTGG	TATTCAAAGC	AATCAGGCGA	ATCCGTTATT	GTTTCTCCCG	ATGTAAAAGG	4380
TACTGTTACT	GTATATTCAT	CTGACGTTAA	ACCTGAAAAT	CTACGCAATT	TCTTTATTTT	4440
TGTTTTACGT	GCTAATAATT	TTGATATGGT	TGGTTCAATT	CCTTCCATAA	TTCAGAAGTA	4500
TAATCCAAAC	AATCAGGATT	ATATTGATGA	ATTGCCATCA	TCTGATAATC	AGGAATATGA	4560
TGATAATTCC	GCTCCTTCTG	GTGGTTTCTT	TGTTCCGCAA	AATGATAATG	TTACTCAAAC	4620
TTTTAAATT	AATAACGTTT	GGGCAAAGGA	TTAATACGA	GTTGTCGAAT	TGTTTGTAAG	4680
GTCTAATACT	TCTAAATCCT	CAAATGTATT	ATCTATTGAC	GGCTCTAATC	TATTAGTTGT	4740
TAGTGCACCT	AAAGATATTT	TAGATAACCT	TCCTCAATTC	CTTTCTACTG	TTGATTTGCC	4800
AACTGACCAG	ATATTGATTG	AGGGTTTGAT	ATTTGAGGTT	CAGCAAGGTG	ATGCTTTAGA	4860
TTTTTCATTT	GCTGCTGGCT	CTCAGCGTGG	CACGTGTTGCA	GGCGGTGTTA	ATACTGACCG	4920
CCTCACCTCT	GTTTTATCTT	CTGCTGGTGG	TTCGTTCCGT	ATTTTAAATG	GCGATGTTTT	4980
AGGGCTATCA	GTTTCGCGCAT	TAAAGACTAA	TAGCCATTCA	AAAATATTGT	CTGTGCCACG	5040
TATTCTTACG	CTTTCAGGTC	AGAAGGGTTC	TATCTCTGTT	GGCCAGAATG	TCCCTTTTAT	5100
TACTGGTCGT	GTGACTGGTG	AATCTGCCAA	TGTAAATAAT	CCATTTTCTG	CGATTGAGCG	5160
TCAAAATGTA	GGTATTTCCA	TGAGCGTTTT	TCCTGTTGCA	ATGGCTGGCG	GTAATATTGT	5220
TCTGGATATT	ACCAGCAAGG	CCGATAGTTT	GAGTTCTTCT	ACTCAGGCAA	GTGATGTTAT	5280

TACTAATCAA	AGAAGTATTG	CTACAACGGT	TAATTTGCGT	GATGGACAGA	CTCTTTTACT	5340
CGGTGGCCTC	ACTGATTATA	AAAACACTTC	TCAAGATTCT	GGCGTACCGT	TCCTGTCTAA	5400
AATCCCTTTA	ATCGGCCTCC	TGTTTAGCTC	CCGCTCTGAT	TCCAACGAGG	AAAGCACGTT	5460
ATACGTGCTC	GTCAAAGCAA	CCATAGTAGC	CGCCCTGTAG	CGGCGCATT	AGCGCGGCGG	5520
GTGTGGTGGT	TACGCGCAGC	GTGACCGCTA	CACTTGCCAG	CGCCCTAGCG	CCCGCTCCTT	5580
TCGCTTTCTT	CCCTTCCTTT	CTCGCCACGT	TCGCCGGCTT	TCCCCGTCAA	GCTCTAAATC	5640
GGGGGCTCCC	TTTAGGGTTC	CGATTTAGTG	CTTTACGGCA	CCTCGACCCC	AAAAAACTTG	5700
ATTTGGGTGA	TGGTTCACGT	AGTGGGCCAT	CGCCCTGATA	GACGGTTTTT	CGCCCTTTGA	5760
CGTTGGAGTC	CACGTTCTTT	AATAGTGGAC	TCTTGTTCCA	AACTGGAACA	ACACTCAACC	5820
CTATCTCGGG	CTATTCTTTT	GATTTATAAG	GGATTTTGCC	GATTTCTGGAA	CCACCATCAA	5880
ACAGGATTTT	CGCCTGCTGG	GGCAAACCAG	CGTGGACCGC	TTGCTGCAAC	TCTCTCAGGG	5940
CCAGGCGGTG	AAGGGCAATC	AGCTGTTGCC	CGTCTCGCTG	GTGAAAAGAA	AAACCACCCT	6000
GGCGCCCAAT	ACGCAAACCG	CCTCTCCCCG	CGCGTTGGCC	GATTCATTAA	TGCAGCTGGC	6060
ACGACAGGTT	TCCCGACTGG	AAAGCGGGCA	GTGAGCGCAA	CGCAATTAAT	GTGAGTTAGC	6120
TCACTCATTA	GGCACCCAG	GCTTTACACT	TTATGCTTCC	GGCTCGTATG	TTGTGTGGAA	6180
TTGTGAGCGG	ATAACAATTT	CACACGCGTC	ACTTGGCACT	GGCCGTCGTT	TTACAACGTC	6240
GTGACTGGGA	AAACCCTGGC	GTTACCCAAG	CTTTGTACAT	GGAGAAAATA	AAGTGAAACA	6300
AAGCACTATT	GCACTGGCAC	TCTTACCGTT	ACCGTTACTG	TTTACCCCTG	TGACAAAAGC	6360
CGCCCAGGTC	CAGCTGCTCG	AGTCAGGCCT	ATTGTGCCCA	GGGGATTGTA	CTAGTGGATC	6420
CTAGGCTGAA	GGCGATGACC	CTGCTAAGGC	TGCATTCAAT	AGTTTACAGG	CAAGTGCTAC	6480
TGAGTACATT	GGCTACGCTT	GGGCTATGGT	AGTAGTTATA	GTTGGTGCTA	CCATAGGGAT	6540
TAAATTATTC	AAAAAGTTTA	CGAGCAAGGC	TTCTTAAGCA	ATAGCGAAGA	GGCCCGCACC	6600
GATCGCCCTT	CCCAACAGTT	GCGCAGCCTG	AATGGCGAAT	GGCGCTTTGC	CTGGTTTCCG	6660
GCACCAGAAG	CGGTGCCGGA	AAGCTGGCTG	GAGTGCGATC	TTCTGAGGC	CGATACGGTC	6720
GTCGTCCCCT	CAAACCTGGCA	GATGCACGGT	TACGATGCGC	CCATCTACAC	CAACGTAACC	6780
TATCCCATTA	CGGTCAATCC	GCCGTTTGTT	CCCACGGAGA	ATCCGACGGG	TTGTTACTCG	6840
CTCACATTTA	ATGTTGATGA	AAGCTGGCTA	CAGGAAGGCC	AGACGCGAAT	TATTTTTGAT	6900
GGCGTTCCCTA	TTGGTTAAAA	AATGAGCTGA	TTTAACAAAA	ATTTAACGCG	AATTTTAACA	6960
AAATATTAAC	GTTTACAATT	TAAATATTTG	CTTATACAAT	CTTCCTGTTT	TTGGGGCTTT	7020
TCTGATTATC	AACCGGGGTA	CATATGATTG	ACATGCTAGT	TTTACGATTA	CCGTTTCATCG	7080
ATTCTCTTGT	TTGCTCCAGA	CTCTCAGGCA	ATGACCTGAT	AGCCTTTGTA	GATCTCTCAA	7140
AAATAGCTAC	CCTCTCCGGC	ATTAATTTAT	CAGCTAGAAC	GGTTGAATAT	CATATTGATG	7200
GTGATTTGAC	TGTCTCCGGC	CTTTCTCACC	CTTTTGAATC	TTTACCTACA	CATTACTCAG	7260
GCATTGCATT	TAAAATATAT	GAGGGTTCTA	AAAATTTTTTA	TCCTTGCGTT	GAAATAAAGG	7320

CTTCTCCCGC	AAAAGTATTA	CAGGGTCATA	ATGTTTTTGG	TACAACCGAT	TTAGCTTTAT	7380
GCTCTGAGGC	TTTATTGCTT	AATTTTGCTA	ATTCTTTGCC	TTGCCTGTAT	GATTTATTGG	7440
ACGTT						7445

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: circular

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AATGCTACTA	CTATTAGTAG	AATTGATGCC	ACCTTTTCAG	CTCGCGCCCC	AAATGAAAAT	60
ATAGCTAAAC	AGGTTATTGA	CCATTTGCGA	AATGTATCTA	ATGGTCAAAC	TAAATCTACT	120
CGTTCGCAGA	ATTGGGAATC	AACTGTTACA	TGGAATGAAA	CTTCCAGACA	CCGTACTTTA	180
GTTGCATATT	TAAAACATGT	TGAGCTACAG	CACCAGATTC	AGCAATTAAG	CTCTAAGCCA	240
TCTGCAAAA	TGACCTCTTA	TCAAAAGGAG	CAATTAAAGG	TACTCTCTAA	TCCTGACCTG	300
TTGGAGTTTG	CTTCCGGTCT	GGTTCGCTTT	GAAGCTCGAA	TTAAAACGCG	ATATTTGAAG	360
TCTTTCGGGC	TTCCTCTTAA	TCTTTTGTAT	GCAATCCGCT	TTGCTTCTGA	CTATAATAGT	420
CAGGGTAAAG	ACCTGATTTT	TGATTTATGG	TCATTCTCGT	TTTCTGAACT	GTTTAAAGCA	480
TTTGAGGGGG	ATTCAATGAA	TATTTATGAC	GATTCCGCAG	TATTGGACGC	TATCCAGTCT	540
AAACATTTTA	CTATTACCCC	CTCTGGCAAA	ACTTCTTTTG	CAAAAGCCTC	TCGCTATTTT	600
GGTTTTTATC	GTCGTCTGGT	AAACGAGGGT	TATGATAGTG	TTGCTCTTAC	TATGCCTCGT	660
AATTCCTTTT	GGCGTTATGT	ATCTGCATTA	GTTGAATGTG	GTATTCCTAA	ATCTCAACTG	720
ATGAATCTTT	CTACCTGTAA	TAATGTTGTT	CCGTTAGTTC	GTTTTATTAA	CGTAGATTTT	780
TCTTCCCAAC	GTCCTGACTG	GTATAATGAG	CCAGTTCTTA	AAATCGCATA	AGGTAATTCA	840
CAATGATTAA	AGTTGAAATT	AAACCATCTC	AAGCCCAATT	TACTACTCGT	TCTGGTGTTT	900
CTCGTCAGGG	CAAGCCTTAT	TCACTGAATG	AGCAGCTTTG	TTACGTTGAT	TTGGGTAATG	960
AATATCCGGT	TCTTGTCAG	ATTACTCTTG	ATGAAGGTCA	GCCAGCCTAT	GCGCCTGGTC	1020
TGTACACCGT	TCATCTGTCC	TCTTTCAAAG	TTGGTCAGTT	CGGTTCCCTT	ATGATTGACC	1080
GTCTGCGCCT	CGTTCCGGCT	AAGTAACATG	GAGCAGGTCT	CGGATTTCGA	CACAATTTAT	1140
CAGGCGATGA	TACAAATCTC	CGTTGTACTT	TGTTTCGCGC	TTGGTATAAT	CGCTGGGGGT	1200
CAAAGATGAG	TGTTTTAGTG	TATTCTTTTC	CCTCTTTTCG	TTTGGTTTGG	TGCCTTCGTA	1260
GTGGCATTAC	GTATTTTACC	CGTTTAATGG	AACTTCCTC	ATGAAAAAGT	CTTTAGTCCT	1320
CAAAGCCTCT	GTAGCCGTTG	CTACCCTCGT	TCCGATGCTG	TCTTTCGCTG	CTGAGGGTGA	1380
CGATCCCGCA	AAAGCGGCCT	TTAACTCCCT	GCAAGCCTCA	GCGACCGAAT	ATATCGGTTA	1440
TGCGTGGGCG	ATGGTTGTTG	TCATTGTCGG	CGCAACTATC	GGTATCAAGC	TGTTTAAGAA	1500

ATTCACCTCG	AAAGCAAGCT	GATAAACCGA	TACAATTAAA	GGCTCCTTTT	GGAGCCTTTT	1560
TTTTTGGAGA	TTTTCAACGT	GAAAAAATTA	TTATTCGCAA	TTCCTTTAGT	TGTTCCCTTTC	1620
TATTCTCACT	CCGCTGAAAC	TGTTGAAAGT	TGTTTAGCAA	AACCCCATAC	AGAAAATTCA	1680
TTTACTAACG	TCTGGAAAGA	CGACAAACT	TTAGATCGTT	ACGCTAACTA	TGAGGGTTGT	1740
CTGTGGAATG	CTACAGGCGT	TGTAGTTTGT	ACTGGTGACG	AAACTCAGTG	TTACGGTACA	1800
TGGGTTCTTA	TTGGGCTTGC	TATCCCTGAA	AATGAGGGTG	GTGGCTCTGA	GGGTGGCGGT	1860
TCTGAGGGTG	GCGGTTCTGA	GGGTGGCGGT	ACTAAACCTC	CTGAGTACGG	TGATACACCT	1920
ATTCCGGGCT	ATACTTATAT	CAACCCTCTC	GACGGCACTT	ATCCGCCTGG	TACTGAGCAA	1980
AACCCCGCTA	ATCCTAATCC	TTCTCTTGAG	GAGTCTCAGC	CTCTTAATAC	TTTCATGTTT	2040
CAGAATAATA	GGTTCCGAAA	TAGGCAGGGG	GCATTAACTG	TTTATACGGG	CACTGTTACT	2100
CAAGGCACTG	ACCCCGTTAA	AAC TTATTAC	CAGTACACTC	CTGTATCATC	AAAAGCCATG	2160
TATGACGCTT	ACTGGAACGG	TAAATTCAGA	GACTGCGCTT	TCCATTCTGG	CTTTAATGAA	2220
GATCCATTCTG	TTTGTGAATA	TCAAGGCCAA	TCGTCTGACC	TGCCTCAACC	TCCTGTCAAT	2280
GCTGGCGGCG	GCTCTGGTGG	TGGTCTGGT	GGCGGCTCTG	AGGGTGGTGG	CTCTGAGGGT	2340
GGCGGTTCTG	AGGGTGGCGG	CTCTGAGGGA	GGCGGTTCCG	GTGGTGGCTC	TGGTTCCGGT	2400
GATTTTGATT	ATGAAAAGAT	GGCAAACGCT	AATAAGGGGG	CTATGACCGA	AAATGCCGAT	2460
GAAAACGCGC	TACAGTCTGA	CGCTAAAGGC	AAACTTGATT	CTGTCGCTAC	TGATTACGGT	2520
GCTGCTATCG	ATGGTTTCAT	TGGTGACGTT	TCCGGCCTTG	CTAATGGTAA	TGGTGCTACT	2580
GGTGATTTTG	CTGGCTCTAA	TTCCCAAATG	GCTCAAGTCG	GTGACGGTGA	TAATTCACCT	2640
TTAATGAATA	ATTTCCGTCA	ATATTTACCT	TCCCTCCCTC	AATCGGTTGA	ATGTCGCCCT	2700
TTTGTCTTTA	GCGCTGGTAA	ACCATATGAA	TTTTCTATTG	ATTGTGACAA	AATAAACTTA	2760
TTCCGTGGTG	TCTTTGCGTT	TCTTTTATAT	GTTGCCACCT	TTATGTATGT	ATTTTCTACG	2820
TTTGCTAACA	TACTGCGTAA	TAAGGAGTCT	TAATCATGCC	AGTTCTTTTG	GGTATTCCGT	2880
TATTATTGCG	TTTCCTCGGT	TTCCTTCTGG	TAAC TTTGTT	CGGCTATCTG	CTTACTTTTC	2940
TTAAAAAGGG	CTTCGGTAAG	ATAGCTATTG	CTATTTTATT	GTTTCTTGCT	CTTATTATTG	3000
GGCTTAACTC	AATTCTTGTT	GGTTATCTCT	CTGATATTAG	CGCTCAATTA	CCCTCTGACT	3060
TTGTTTCAGGG	TGTTTCAGTTA	ATTCTCCCGT	CTAATGCGCT	TCCCTGTTTT	TATGTTATTTC	3120
TCTCTGTAAA	GGCTGCTATT	TTCATTTTTG	ACGTTAACAA	AAAAATCGTT	TCTTATTTGG	3180
ATTGGGATAA	ATAATATGGC	TGTTTATTTT	GTAAC TGGCA	AATTAGGCTC	TGGAAAGACG	3240
CTCGTTAGCG	TTGGTAAGAT	TCAGGATAAA	ATTGTAGCTG	GGTGCAAAAT	AGCAACTAAT	3300
CTTGATTTAA	GGCTTCAAAA	CCTCCCGCAA	GTCGGGAGGT	TCGCTAAAAC	GCCTCGCGTT	3360
CTTAGAATAC	CGGATAAGCC	TTCTATATCT	GATTTGCTTG	CTATTGGGCG	CGGTAATGAT	3420
TCCTACGATG	AAAATAAAAA	CGGCTTGCTT	GTTCTCGATG	AGTGC GG TAC	TTGGTTTAAAT	3480
ACCCGTTCTT	GGAATGATAA	GGAAAGACAG	CCGATTATTG	ATTGGTTTCT	ACATGCTCGT	3540

AAATTAGGAT	GGGATATTAT	TTTTCTTGTT	CAGGACTTAT	CTATTGTTGA	TAAACAGGCG	3600
CGTTCTGCAT	TAGCTGAACA	TGTTGTTTAT	TGTCGTCGTC	TGGACAGAAT	TACTTTACCT	3660
TTTGTCGGTA	CTTTATATTC	TCTTATTACT	GGCTCGAAAA	TGCCTCTGCC	TAAATTACAT	3720
GTTGGCGTTG	TTAAATATGG	CGATTCTCAA	TTAAGCCCTA	CTGTTGAGCG	TTGGCTTTAT	3780
ACTGGTAAGA	ATTTGTATAA	CGCATATGAT	ACTAAACAGG	CTTTTTCTAG	TAATTATGAT	3840
TCCGGTGTTT	ATTCTTATTT	AACGCCTTAT	TTATCACACG	GTCGGTATTT	CAAACCATTA	3900
AATTTAGGTC	AGAAGATGAA	GCTTACTAAA	ATATATTTGA	AAAAGTTTTT	ACGCGTTCTT	3960
TGTCTTGCGA	TTGGATTTGC	ATCAGCATTT	ACATATAGTT	ATATAACCCA	ACCTAAGCCG	4020
GAGGTTAAAA	AGGTAGTCTC	TCAGACCTAT	GATTTTGATA	AATTCACTAT	TGACTCTTCT	4080
CAGCGTCTTA	ATCTAAGCTA	TCGCTATGTT	TTCAAGGATT	CTAAGGGAAA	ATTAATTAAT	4140
AGCGACGATT	TACAGAAGCA	AGGTTATTCA	CTCACATATA	TTGATTTATG	TACTGTTTCC	4200
ATTAAAAAAG	GTAATTCAAA	TGAAATTGTT	AAATGTAATT	AATTTTGTTT	TCTTGATGTT	4260
TGTTTCATCA	TCTTCTTTTG	CTCAGGTAAT	TGAAATGAAT	AATTCGCCTC	TGCGCGATTT	4320
TGTAACCTGG	TATTCAAAGC	AATCAGGCGA	ATCCGTTATT	GTTTCTCCCG	ATGTAAAAGG	4380
TACTGTTACT	GTATATTCAT	CTGACGTTAA	ACCTGAAAAT	CTACGCAATT	TCTTTATTTT	4440
TGTTTTACGT	GCTAATAATT	TTGATATGGT	TGGTTCAATT	CCTTCCATAA	TTCAGAAGTA	4500
TAATCCAAAC	AATCAGGATT	ATATTGATGA	ATTGCCATCA	TCTGATAATC	AGGAATATGA	4560
TGATAATTCC	GCTCCTTCTG	GTGGTTTCTT	TGTTCCGCAA	AATGATAATG	TTACTCAAAC	4620
TTTTAAAATT	AATAACGTTT	GGGCAAAGGA	TTTAATACGA	GTTGTCGAAT	TGTTTGTAAG	4680
GTCTAATACT	TCTAAATCCT	CAAATGTATT	ATCTATTGAC	GGCTCTAATC	TATTAGTTGT	4740
TAGTGCACCT	AAAGATATTT	TAGATAACCT	TCCTCAATTC	CTTCTACTTG	TTGATTTGCC	4800
AACTGACCAG	ATATTGATTG	AGGGTTTGAT	ATTTGAGGTT	CAGCAAGGTG	ATGCTTTAGA	4860
TTTTTCATTT	GCTGCTGGCT	CTCAGCGTGG	CACTGTTGCA	GGCGGTGTTA	ATACTGACCG	4920
CCTCACCTCT	GTTTTATCTT	CTGCTGGTGG	TTGTTTCGGT	ATTTTAAATG	GCGATGTTTT	4980
AGGGCTATCA	GTTTCGCGCAT	TAAAGACTAA	TAGCCATTCA	AAAATATTGT	CTGTGCCACG	5040
TATTCTTACG	CTTTCAGGTC	AGAAGGGTTC	TATCTCTGTT	GCCAGAATG	TCCCTTTTAT	5100
TACTGGTCGT	GTGACTGGTG	AATCTGCCAA	TGTAAATAAT	CCATTTTACA	CGATTGAGCG	5160
TCAAAATGTA	GGTATTTCCA	TGAGCGTTTT	TCCTGTTGCA	ATGGCTGGCG	GTAATATTGT	5220
TCTGGATATT	ACCAGCAAGG	CCGATAGTTT	GAGTTCTTCT	ACTCAGGCAA	GTGATGTTAT	5280
TACTAATCAA	AGAAGTATTG	CTACAACGGT	TAATTTGCGT	GATGGACAGA	CTCTTTTACT	5340
CGGTGGCCTC	ACTGATTATA	AAAACACTTC	TCAAGATTCT	GGCGTACCGT	TCCTGTCTAA	5400
AATCCCTTTA	ATCGGCCTCC	TGTTTAGCTC	CCGCTCTGAT	TCCAACGAGG	AAAGCACGTT	5460
ATACGTGCTC	GTCAAAGCAA	CCATAGTACG	CGCCCTGTAG	CGGCGCATTA	AGCGCGGCGG	5520
GTGTGGTGGT	TACGCGCAGC	GTGACCGCTA	CACTTGCCAG	CGCCCTAGCG	CCCCTCCTT	5580

TCGCTTTCTT	CCCTTCCTTT	CTCGCCACGT	TCGCCGGCTT	TCCCCGTCAA	GCTCTAAATC	5640
GGGGGCTCCC	TTAGGGTTC	CGATTTAGTG	CTTTACGGCA	CCTCGACCCC	AAAAAAGTTG	5700
ATTTGGGTGA	TGGTTCACGT	AGTGGGCCAT	CGCCCTGATA	GACGGTTTTT	CGCCCTTTGA	5760
CGTTGGAGTC	CACGTTCTTT	AATAGTGGAC	TCTTGTTCCA	AACTGGAACA	ACACTCAACC	5820
CTATCTCGGG	CTATTCTTTT	GATTTATAAG	GGATTTTGCC	GATTTCGGAA	CCACCATCAA	5880
ACAGGATTTT	CGCCTGCTGG	GGCAAACCAG	CGTGGACCGC	TTGCTGCAAC	TCTCTCAGGG	5940
CCAGGCGGTG	AAGGGCAATC	AGCTGTTGCC	CGTCTCGCTG	GTGAAAAGAA	AAACCACCCT	6000
GGCGCCCAAT	ACGCAAACCG	CCTCTCCCCG	CGCGTTGGCC	GATTCATTAA	TGCAGCTGGC	6060
ACGACAGGTT	TCCCGACTGG	AAAGCGGGCA	GTGAGCGCAA	CGCAATTAAT	GTGAGTTAGC	6120
TCACTCATTA	GGCACCCAG	GCTTTACACT	TTATGCTTCC	GGCTCGTATG	TTGTGTGGAA	6180
TTGTGAGCGG	ATAACAATTT	CACACGCGTC	ACTTGGCACT	GGCCGTCGTT	TTACAACGTC	6240
GTGACTGGGA	AAACCCTGGC	GTTACCCAAG	CTTTGTACAT	GGAGAAAATA	AAGTGAAACA	6300
AAGCACTATT	GCACTGGCAC	TCTTACCGTT	ACTGTTTACC	CCTGTGGCAA	AAGCCTATGG	6360
GGGGTTTATG	ACTTCTGAGG	GATCCGGAGC	TGAAGGCGAT	GACCCTGCTA	AGGCTGCATT	6420
CAATAGTTTA	CAGGCAAGTG	CTACTGAGTA	CATTGGCTAC	GCTTGGGCTA	TGGTAGTAGT	6480
TATAGTTGGT	GCTACCATAG	GGATTAAATT	ATTCAAAAAG	TTTACGAGCA	AGGCTTCTTA	6540
AGCAATAGCG	AAGAGGCCCG	CACCGATCGC	CCTTCCCAAC	AGTTGCGCAG	CCTGAATGGC	6600
GAATGGCGCT	TTGCCTGGTT	TCCGGCACCA	GAAGCGGTGC	CGGAAAGCTG	GCTGGAGTGC	6660
GATCTTCCTG	AGGCCGATAC	GGTCGTCGTC	CCCTCAAAC	GGCAGATGCA	CGGTTACGAT	6720
GCGCCCATCT	ACACCAACGT	AACCTATCCC	ATTACGGTCA	ATCCGCCGTT	TGTTCCCACG	6780
GAGAATCCGA	CGGGTTGTTA	CTCGCTCACA	TTTAATGTTG	ATGAAAGCTG	GCTACAGGAA	6840
GGCCAGACGC	GAATTATTTT	TGATGGCGTT	CCTATTGGTT	AAAAAATGAG	CTGATTTAAC	6900
AAAAATTTAA	CGCGAATTTT	AACAAAATAT	TAACGTTTAC	AATTTAAATA	TTTGCTTATA	6960
CAATCTTCCT	GTTTTTGGGG	CTTTTCTGAT	TATCAACCGG	GGTACATATG	ATTGACATGC	7020
TAGTTTTACG	ATTACCGTTC	ATCGATTCTC	TTGTTTGCTC	CAGACTCTCA	GGCAATGACC	7080
TGATAGCCTT	TGTAGATCTC	TCAAAAATAG	CTACCCTCTC	CGGCATTAAT	TTATCAGCTA	7140
GAACGGTTGA	ATATCATATT	GATGGTGATT	TGACTGTCTC	CGGCCTTTCT	CACCCTTTTG	7200
AATCTTTACC	TACACATTAC	TCAGGCATTG	CATTTAAAT	ATATGAGGGT	TCTAAAAAAT	7260
TTTATCCTTG	CGTTGAAATA	AAGGCTTCTC	CCGCAAAAGT	ATTACAGGGT	CATAATGTTT	7320
TTGGTACAAC	CGATTTAGCT	TTATGCTCTG	AGGCTTTATT	GCTTAATTTT	GCTAATTCTT	7380
TGCCTTGCCT	GTATGATTTA	TTGGACGTT				7409

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: circular

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AATGCTACTA	CTATTAGTAG	AATTGATGCC	ACCTTTTCAG	CTCGCGCCCC	AAATGAAAAT	60
ATAGCTAAAC	AGGTTATTGA	CCATTTGCGA	AATGTATCTA	ATGGTCAAAC	TAAATCTACT	120
CGTTGCGAGA	ATTGGGAATC	AACTGTTACA	TGGAATGAAA	CTTCCAGACA	CCGTACTTTA	180
GTTGCATATT	TAAAACATGT	TGAGCTACAG	CACCAGATTC	AGCAATTAAG	CTCTAAGCCA	240
TCTGCAAAAA	TGACCTCTTA	TCAAAAGGAG	CAATTAAAGG	TACTCTCTAA	TCCTGACCTG	300
TTGGAGTTTG	CTTCCGGTCT	GGTTCGCTTT	GAAGCTCGAA	TTAAACGCG	ATATTTGAAG	360
TCTTTCGGGC	TTCCTCTTAA	TCTTTTGTAT	GCAATCCGCT	TTGCTTCTGA	CTATAATAGT	420
CAGGGTAAAG	ACCTGATTTT	TGATTTATGG	TCATTCTCGT	TTTCTGAACT	GTTTAAAGCA	480
TTTGAGGGGG	ATTCAATGAA	TATTTATGAC	GATTCCGCAG	TATTGGACGC	TATCCAGTCT	540
AAACATTTTA	CTATTACCCC	CTCTGGCAAA	ACTTCTTTTG	CAAAAGCCTC	TCGCTATTTT	600
GGTTTTTATC	GTCGTCTGGT	AAACGAGGGT	TATGATAGTG	TTGCTCTTAC	TATGCCTCGT	660
AATTCCTTTT	GGCGTTATGT	ATCTGCATTA	GTTGAATGTG	GTATTCCTAA	ATCTCAACTG	720
ATGAATCTTT	CTACCTGTAA	TAATGTTGTT	CCGTTAGTTC	GTTTTATTAA	CGTAGATTTT	780
TCTTCCCAAC	GTCCTGACTG	GTATAATGAG	CCAGTTCTTA	AAATCGCATA	AGGTAATTCA	840
CAATGATTAA	AGTTGAAATT	AAACCATCTC	AAGCCCAATT	TACTACTCGT	TCTGGTGTTT	900
CTCGTCAGGG	CAAGCCTTAT	TCACTGAATG	AGCAGCTTTG	TTACGTTGAT	TTGGGTAATG	960
AATATCCGGT	TCTTGTCAG	ATTACTCTTG	ATGAAGGTCA	GCCAGCCTAT	GCGCCTGGTC	1020
TGTACACCGT	TCATCTGTCC	TCTTTCAAAG	TTGGTCAGTT	CGGTTCCCTT	ATGATTGACC	1080
GTCTGCGCCT	CGTTCCGGCT	AAGTAACATG	GAGCAGGTCG	CGGATTTCGA	CACAATTTAT	1140
CAGGCGATGA	TACAAATCTC	CGTTGTACTT	TGTTTCGCGC	TTGGTATAAT	CGCTGGGGGT	1200
CAAAGATGAG	TGTTTTAGTG	TATTCTTTTCG	CCTCTTTTCGT	TTTAGGTTGG	TGCCTTCGTA	1260
GTGGCATTAC	GTATTTTACC	CGTTTAATGG	AAACTTCCTC	ATGAAAAAGT	CTTTAGTCCT	1320
CAAAGCCTCT	GTAGCCGTTG	CTACCCTCGT	TCCGATGCTG	TCTTTCGCTG	CTGAGGGTGA	1380
CGATCCCGCA	AAAGCGGCCT	TTAACTCCCT	GCAAGCCTCA	GCGACCGAAT	ATATCGGTTA	1440
TGCGTGCGCG	ATGGTTGTTG	TCATTGTGCG	CGCAACTATC	GGTATCAAGC	TGTTTAAGAA	1500
ATTCACCTCG	AAAGCAAGCT	GATAAACCGA	TACAATTAAA	GGCTCCTTTT	GGAGCCTTTT	1560
TTTTTGAGAG	TTTTCAACGT	GAAAAAATTA	TTATTCGCAA	TTCTTTTAGT	TGTTCCCTTC	1620
TATTCTCACT	CCGCTGAAAC	TGTTGAAAGT	TGTTTAGCAA	AACCCCATAC	AGAAAATTCA	1680

TTTACTAACG	TCTGGAAAGA	CGACAAAAC	TTAGATCGTT	ACGCTAACTA	TGAGGGTTGT	1740
CTGTGGAATG	CTACAGGCGT	TGTAGTTTGT	ACTGGTGACG	AAACTCAGTG	TTACGGTACA	1800
TGGGTTCCTA	TTGGGCTTGC	TATCCCTGAA	AATGAGGGTG	GTGGCTCTGA	GGGTGGCGGT	1860
TCTGAGGGTG	GCGGTTCTGA	GGGTGGCGGT	ACTAAACCTC	CTGAGTACGG	TGATACACCT	1920
ATTCCGGGCT	ATACTTATAT	CAACCCTCTC	GACGGCACTT	ATCCGCCTGG	TACTGAGCAA	1980
AACCCCGCTA	ATCCTAATCC	TTCTCTTGAG	GAGTCTCAGC	CTCTTAATAC	TTTCATGTTT	2040
CAGAATAATA	GGTTCCGAAA	TAGGCAGGGG	GCATTAAC	TTTATACGGG	CACGTGTTACT	2100
CAAGGCACTG	ACCCCGTTAA	AACTTATTAC	CAGTACACTC	CTGTATCATC	AAAAGCCATG	2160
TATGACGCTT	ACTGGAACGG	TAAATTGAGA	GACTGCGCTT	TCCATTCTGG	CTTTAATGAA	2220
GATCCATTCTG	TTTGTGAATA	TCAAGGCCAA	TCGTCTGACC	TGCCTCAACC	TCCTGTCAAT	2280
GCTGGCGGCG	GCTCTGGTGG	TGGTTCTGGT	GGCGGCTCTG	AGGGTGGTGG	CTCTGAGGGT	2340
GGCGGTTCTG	AGGGTGGCGG	CTCTGAGGGA	GGCGGTTCCG	GTGGTGGCTC	TGGTTCGGGT	2400
GATTTTGATT	ATGAAAAGAT	GGCAAACGCT	AATAAGGGGG	CTATGACCGA	AAATGCCGAT	2460
GAAAACGCGC	TACAGTCTGA	CGCTAAAGGC	AAACTTGATT	CTGTCGCTAC	TGATTACGGT	2520
GCTGCTATCG	ATGGTTTCAT	TGGTGACGTT	TCCGGCCTTG	CTAATGGTAA	TGGTGCTACT	2580
GGTGATTTTG	CTGGCTCTAA	TTCCCAAATG	GCTCAAGTCG	GTGACGGTGA	TAATTCACCT	2640
TTAATGAATA	ATTTCCGTCA	ATATTTACCT	TCCCTCCCTC	AATCGGTTGA	ATGTCGCCCT	2700
TTTGTCTTTA	GCGCTGGTAA	ACCATATGAA	TTTCTATTG	ATTGTGACAA	AATAAACTTA	2760
TTCCGTGGTG	TCTTTGCGTT	TCTTTTATAT	GTTGCCACCT	TTATGTATGT	ATTTTCTACG	2820
TTTGCTAACA	TACTGCGTAA	TAAGGAGTCT	TAATCATGCC	AGTTCTTTTG	GGTATTCCGT	2880
TATTATTGCG	TTTCCTCGGT	TTCCTTCTGG	TAACTTTGTT	CGGCTATCTG	CTTACTTTTC	2940
TTAAAAAGGG	CTTCGGTAAG	ATAGCTATTG	CTATTTTCATT	GTTTCTTGCT	CTTATTATTG	3000
GGCTTAACTC	AATTCTTGTTG	GGTTATCTCT	CTGATATTAG	CGCTCAATTA	CCCTCTGACT	3060
TTGTTTCAGGG	TGTTTCAGTTA	ATTCTCCCGT	CTAATGCGCT	TCCCTGTTTT	TATGTTATTC	3120
TCTCTGTAAA	GGCTGCTATT	TTCATTTTTG	ACGTAAACA	AAAAATCGTT	TCTTATTTGG	3180
ATTGGGATAA	ATAATATGGC	TGTTTATTTT	GTAACGGCA	AATTAGGCTC	TGGAAAGACG	3240
CTCGTTAGCG	TTGGTAAGAT	TCAGGATAAA	ATTGTAGCTG	GGTGCAAAAT	AGCAACTAAT	3300
CTTGATTTAA	GGCTTCAAAA	CCTCCCGCAA	GTCGGGAGGT	TCGCTAAAAC	GCCTCGCGTT	3360
CTTAGAATAC	CGGATAAGCC	TTCTATATCT	GATTTGCTTG	CTATTGGGCG	CGGTAATGAT	3420
TCCTACGATG	AAAATAAAAA	CGGCTTGCTT	GTTCTCGATG	AGTGCGGTAC	TTGGTTTAAT	3480
ACCCGTTCTT	GGAATGATAA	GGAAAGACAG	CCGATTATTG	ATTGGTTTCT	ACATGCTCGT	3540
AAATTAGGAT	GGGATATTAT	CTTCCTTGTT	CAGGACTTAT	CTATTGTTGA	TAAACAGGCG	3600
CGTTCTGCAT	TAGCTGAACA	TGTTGTTTAT	TGTCGTCGTC	TGGACAGAAT	TACTTTACCT	3660
TTTGTGCGTA	CTTTATATTC	TCTTATTACT	GGCTCGAAAA	TGCCTCTGCC	TAAATTACAT	3720

GTTGGCGTTG	TTAAATATGG	CGATTCTCAA	TTAAGCCCTA	CTGTTGAGCG	TTGGCTTTAT	3780
ACTGGTAAGA	ATTTGTATAA	CGCATATGAT	ACTAAACAGG	CTTTTTCTAG	TAATTATGAT	3840
TCCGGTGTTT	ATTCTTATTT	AACGCCTTAT	TTATCACACG	GTCGGTATTT	CAAACCATTA	3900
AATTTAGGTC	AGAAGATGAA	GCTTACTAAA	ATATATTTGA	AAAAGTTTTC	ACGCGTTCCT	3960
TGTCTTGCGA	TTGGATTTGC	ATCAGCATTT	ACATATAGTT	ATATAACCCA	ACCTAAGCCG	4020
GAGGTTAAAA	AGGTAGTCTC	TCAGACCTAT	GATTTTGATA	AATTCACTAT	TGACTCTTCT	4080
CAGCGTCTTA	ATCTAAGCTA	TCGCTATGTT	TTCAAGGATT	CTAAGGGAAA	ATTAATTAAT	4140
AGCGACGATT	TACAGAAGCA	AGGTTATTCA	CTCACATATA	TTGATTTATG	TACTGTTTCC	4200
ATTAAAAAGG	TAATTCAAAT	GAAATTGTTA	AATGTAATTA	ATTTTGTTTT	CTTGATGTTT	4260
GTTTCATCAT	CTTCTTTTGC	TCAGGTAATT	GAAATGAATA	ATTCGCCTCT	GCGCGATTTT	4320
GTAAC TTGGT	ATTCAAAGCA	ATCAGGCGAA	TCCGTTATTG	TTTCTCCCGA	TGTAAAAGGT	4380
ACTGTTACTG	TATATTCATC	TGACGTTAAA	CCTGAAAATC	TACGCAATTT	CTTTATTTCT	4440
GTTTTACGTG	CTAATAATTT	TGATATGGTT	GTTTCAATTC	CTTCCATTAT	TTAGAAGTAT	4500
AATCCAAACA	ATCAGGATTA	TATTGATGAA	TTGCCATCAT	CTGATAATCA	GGAATATGAT	4560
GATAATTCCG	CTCCTTCTGG	TGGTTTCTTT	GTTCCGCAAA	ATGATAATGT	TACTCAAAC	4620
TTTAAAATTA	ATAACGTTCT	GGCAAAGGAT	TTAATACGAG	TTGTCGAATT	GTTTGTAAG	4680
TCTAATACTT	CTAAATCCTC	AAATGTATTA	TCTATTGACG	GCTCTAATCT	ATTAGTTGTT	4740
AGTGACACCTA	AAGATATTTT	AGATAACCTT	CCTCAATTCC	TTTCTACTGT	TGATTTGCCA	4800
ACTGACCAGA	TATTGATTGA	GGGTTTGATA	TTTGAGGTTT	AGCAAGGTGA	TGCTTTAGAT	4860
TTTTCATTTG	CTGCTGGCTC	TCAGCGTGGC	ACTGTTGCAG	GCGGTGTTAA	TACTGACCGC	4920
CTCACCTCTG	TTTTATCTTC	TGCTGGTGGT	TCGTTCCGTA	TTTTTAATGG	CGATGTTTTA	4980
GGGCTATCAG	TTGCGCATT	AAAGACTAAT	AGCCATTCAA	AAATATTGTC	TGTGCCACGT	5040
ATTCTTACGC	TTTCAGGTCA	GAAGGGTTCT	ATCTCTGTTG	GCCAGAATGT	CCCTTTTATT	5100
ACTGGTCGTG	TGACTGGTGA	ATCTGCCAAT	GTAATAATC	CATTCAGAC	GATTGAGCGT	5160
CAAAATGTAG	GTATTTCCAT	GAGCGTTTTT	CCTGTTGCAA	TGGCTGGCGG	TAATATTGTT	5220
CTGGATATTA	CCAGCAAGGC	CGATAGTTTG	AGTTCTTCTA	CTCAGGCAAG	TGATGTTATT	5280
ACTAATCAAA	GAAGTATTGC	TACAACGGTT	AATTTGCGTG	ATGGACAGAC	TCTTTTACTC	5340
GGTGGCCTCA	CTGATTATAA	AAACACTTCT	CAAGATTCTG	GCGTACCGTT	CCTGTCTAAA	5400
ATCCCTTTAA	TCGGCCTCCT	GTTTAGCTCC	CGCTCTGATT	CCAACGAGGA	AAGCACGTTA	5460
TACGTGCTCG	TCAAAGCAAC	CATAGTACGC	GCCCTGTAGC	GGCGCATTA	GCGCGGCGGG	5520
TGTGGTGGTT	ACGCGCAGCG	TGACCGCTAC	ACTTGCCAGC	GCCCTAGCGC	CCGCTCCTTT	5580
CGCTTTCTTC	CCTTCCTTTC	TCGCCACGTT	CGCCGGCTTT	CCCCGTCAAG	CTCTAAATCG	5640
GGGGCTCCCT	TTAGGGTTCC	GATTTAGTGC	TTTACGGCAC	CTCGACCCCA	AAAACTTGA	5700
TTTGGGTGAT	GGTTCACGTA	GTGGGCCATC	GCCCTGATAG	ACGGTTTTTC	GCCCTTTGAC	5760

GTTGGAGTCC	ACGTTCTTTA	ATAGTGGACT	CTTGTTCCAA	ACTGGAACAA	CACTCAACCC	5820
TATCTCGGGC	TATTCTTTTG	ATTTATAAGG	GATTTTGCCG	ATTTCGGAAC	CACCATCAAA	5880
CAGGATTTTC	GCCTGCTGGG	GCAAACCAGC	GTGGACCGCT	TGCTGCAACT	CTCTCAGGGC	5940
CAGGCGGTGA	AGGGCAATCA	GCTGTTGCCC	GTCTCGCTGG	TGAAAAGAAA	AACCACCCTG	6000
GCGCCCAATA	CGCAAACCGC	CTCTCCCCGC	GCGTTGGCCG	ATTCATTAAT	GCAGCTGGCA	6060
CGACAGGTTT	CCCRACTGGA	AAGCGGGCAG	TGAGCGCAAC	GCAATTAATG	TGAGTTAGCT	6120
CACTCATTAG	GCACCCCAGG	CTTTACACTT	TATGCTTCCG	GCTCGTATGT	TGTGTGGAAT	6180
TGTGAGCGGA	TAACAATTTT	ACACAGGAAA	CAGCTATGAC	CAGGATGTAC	GAATTCGCAG	6240
GTAGGAGAGC	TCGGCGGATC	CGAGGCTGAA	GGCGATGACC	CTGCTAAGGC	TGCATTCAAT	6300
AGTTTACAGG	CAAGTGCTAC	TGAGTACATT	GGCTACGCTT	GGGCTATGGT	AGTAGTTATA	6360
GTTGGTGCTA	CCATAGGGAT	TAAATTATTC	AAAAAGTTTA	CGAGCAAGGC	TTCTTAACCA	6420
GCTGGCGTAA	TAGCGAAGAG	GCCCGCACCG	ATCGCCCTTC	CCAACAGTTG	CGCAGCCTGA	6480
ATGGCGAATG	GCGCTTTGCC	TGGTTTCCGG	CACCAGAAGC	GGTGCCGGAA	AGCTGGCTGG	6540
AGTGCGATCT	TCCTGAGGCC	GATACGGTCG	TCGTCCCCTC	AAACTGGCAG	ATGCACGGTT	6600
ACGATGCGCC	CATCTACACC	AACGTAACCT	ATCCCATTAC	GGTCAATCCG	CCGTTTGTTT	6660
CCACGGAGAA	TCCGACGGGT	TGTTACTCGC	TCACATTTAA	TGTTGATGAA	AGCTGGCTAC	6720
AGGAAGGCCA	GACGCGAATT	ATTTTTGATG	GCGTTCCTAT	TGGTTAAAAA	ATGAGCTGAT	6780
TTAACAAAAA	TTTAACGCGA	ATTTTAACAA	AATATTAAACG	TTTACAATTT	AAATATTTGC	6840
TTATACAATC	TTCCTGTTTT	TGGGGCTTTT	CTGATTATCA	ACCGGGGTAC	ATATGATTGA	6900
CATGCTAGTT	TTACGATTAC	CGTTCATCGA	TTCTCTTGTT	TGCTCCAGAC	TCTCAGGCAA	6960
TGACCTGATA	GCCTTTGTAG	ATCTCTCAAA	AATAGCTACC	CTCTCCGGCA	TTAATTTATC	7020
AGCTAGAACG	GTTGAATATC	ATATTGATGG	TGATTTGACT	GTCTCCGGCC	TTTCTCACCC	7080
TTTTGAATCT	TTACCTACAC	ATTACTCAGG	CATTGCATTT	AAAATATATG	AGGGTCTCTAA	7140
AAATTTTTAT	CCTTGCGTTG	AAATAAAGGC	TTCTCCCGCA	AAAGTATTAC	AGGGTCATAA	7200
TGTTTTTGGT	ACAACCGATT	TAGCTTTATG	CTCTGAGGCT	TTATTGCTTA	ATTTTGCTAA	7260
TTCTTTGCCT	TGCCTGTATG	ATTTATTGGA	CGTT			7294

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: circular

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AATGCTACTA	CTATTAGTAG	AATTGATGCC	ACCTTTTCAG	CTCGCGCCCC	AAATGAAAAT	60
ATAGCTAAAC	AGGTTATTGA	CCATTTGCGA	AATGTATCTA	ATGGTCAAAC	TAAATCTACT	120

CGTTTCGCAGA	ATTGGGAATC	AACTGTTACA	TGGAATGAAA	CTTCCAGACA	CCGTACTTTA	180
GTTGCATATT	TAAAACATGT	TGAGCTACAG	CACCAGATTC	AGCAATTAAG	CTCTAAGCCA	240
TCTGCAAAAA	TGACCTCTTA	TCAAAAGGAG	CAATTAAAGG	TACTCTCTAA	TCCTGACCTG	300
TTGGAGTTTG	CTTCCGGTCT	GGTTCGCTTT	GAAGCTCGAA	TTAAAACGCG	ATATTTGAAG	360
TCTTTCGGGC	TTCTCTTAA	TCTTTTTGAT	GCAATCCGCT	TTGCTTCTGA	CTATAATAGT	420
CAGGGTAAAG	ACCTGATTTT	TGATTTATGG	TCATTCTCGT	TTTCTGAACT	GTTTAAAGCA	480
TTTGAGGGGG	ATTCAATGAA	TATTTATGAC	GATTCCGCAG	TATTGGACGC	TATCCAGTCT	540
AAACATTTTA	CTATTACCCC	CTCTGGCAAA	ACTTCTTTTG	CAAAGCCTC	TCGCTATTTT	600
GGTTTTTATC	GTCGTCTGGT	AAACGAGGGT	TATGATAGTG	TTGCTCTTAC	TATGCCTCGT	660
AATTCCTTTT	GGCGTTATGT	ATCTGCATTA	GTTGAATGTG	GTATTCCTAA	ATCTCAACTG	720
ATGAATCTTT	CTACCTGTAA	TAATGTTGTT	CCGTTAGTTC	GTTTTATTAA	CGTAGATTTT	780
TCTTCCCAAC	GTCCTGACTG	GTATAATGAG	CCAGTTCTTA	AAATCGCATA	AGGTAATTCA	840
CAATGATTAA	AGTTGAAATT	AAACCATCTC	AAGCCCAATT	TACTACTCGT	TCTGGTGTTT	900
CTCGTCAGGG	CAAGCCTTAT	TCACTGAATG	AGCAGCTTTG	TTACGTTGAT	TTGGGTAATG	960
AATATCCGGT	TCTTGTC AAG	ATTACTCTTG	ATGAAGGTCA	GCCAGCCTAT	GCGCCTGGTC	1020
TGTACACCGT	TCATCTGTCC	TCTTTC AAG	TTGGTCAGTT	CGGTTCCCTT	ATGATTGACC	1080
GTCTGCGCCT	CGTTCCGGCT	AAGTAACATG	GAGCAGGTG	CGGATTTCTGA	CACAATTTAT	1140
CAGGCGATGA	TACAAATCTC	CGTTGTACTT	TGTTTCGCGC	TTGGTATAAT	CGCTGGGGGT	1200
CAAAGATGAG	TGTTTTAGTG	TATTCTTTCG	CCTCTTTCGT	TTTAGGTTGG	TGCCTTCGTA	1260
GTGGCATTAC	GTATTTTACC	CGTTTAATGG	AAACTTCCTC	ATGAAAAAGT	CTTTAGTCCT	1320
CAAAGCCTCT	GTAGCCGTTG	CTACCCTCGT	TCCGATGCTG	TCTTTCGCTG	CTGAGGGTGA	1380
CGATCCCGCA	AAAGCGGCCT	TTAACTCCCT	GCAAGCCTCA	GCGACC GAAT	ATATCGGTTA	1440
TGCGTG GCG	ATGGTTGTTG	TCATTGTCCG	CGCAACTATC	GGTATCAAGC	TGTTTAAGAA	1500
ATTCACCTCG	AAAGCAAGCT	GATAAACCGA	TACAATTAAA	GGCTCCTTTT	GGAGCCTTTT	1560
TTTTTG GAGA	TTTTCAACGT	GAAAAAATTA	TTATTGCGAA	TTCTTTTAGT	TGTTCTCTTC	1620
TATTCTCACT	CCGCTGAAAC	TGTTGAAAGT	TGTTTAGCAA	AACCCCATAC	AGAAAATTCA	1680
TTTACTAACG	TCTGGAAAGA	CGACAAAAC	TTAGATCGTT	ACGCTAACTA	TGAGGGTTGT	1740
CTGTGGAATG	CTACAGGCGT	TGTAGTTTGT	ACTGGTGACG	AAACTCAGTG	TTACGGTACA	1800
TGGGTTCCTA	TTGGGCTTGC	TATCCCTGAA	AATGAGGGTG	GTGGCTCTGA	GGGTGGCGGT	1860
TCTGAGGGTG	GCGGTTCTGA	GGGTGGCGGT	ACTAAACCTC	CTGAGTACGG	TGATACACCT	1920
ATTCCGGGCT	ATACTTATAT	CAACCCTCTC	GACGGCACTT	ATCCGCCTGG	TACTGAGCAA	1980
AACCCCGCTA	ATCCTAATCC	TTCTCTTGAG	GAGTCTCAGC	CTCTTAATAC	TTTCATGTTT	2040
CAGAATAATA	GGTTCCGAAA	TAGGCAGGGG	GCATTAAC	TTTATACGGG	CACTGTTACT	2100
CAAGGCACTG	ACCCCGTTAA	AACTTATTAC	CAGTACACTC	CTGTATCATC	AAAAGCCATG	2160

TATGACGCTT	ACTGGAACGG	TAAATTCAGA	GACTGCGCTT	TCCATTCTGG	CTTTAATGAA	2220
GATCCATTTCG	TTTGTGAATA	TCAAGGCCAA	TCGTCTGACC	TGCCTCAACC	TCCTGTCAAT	2280
GCTGGCGGCG	GCTCTGGTGG	TGGTTCTGGT	GGCGGCTCTG	AGGGTGGTGG	CTCTGAGGGT	2340
GGCGGTTCTG	AGGGTGGCGG	CTCTGAGGGA	GGCGGTTCCG	GTGGTGGCTC	TGGTTCCGGT	2400
GATTTTGATT	ATGAAAAGAT	GGCAAACGCT	AATAAGGGGG	CTATGACCGA	AAATGCCGAT	2460
GAAAACGCGC	TACAGTCTGA	CGCTAAAGGC	AAACTTGATT	CTGTGCTAC	TGATTACGGT	2520
GCTGCTATCG	ATGGTTTCAT	TGGTGACGTT	TCCGGCCTTG	CTAATGGTAA	TGGTGCTACT	2580
GGTGATTTTG	CTGGCTCTAA	TTCCCAAATG	GCTCAAGTCG	GTGACGGTGA	TAATTCACCT	2640
TTAATGAATA	ATTTCCGTCA	ATATTTACCT	TCCCTCCCTC	AATCGGTTGA	ATGTCGCCCT	2700
TTTGTCTTTA	GCGCTGGTAA	ACCATATGAA	TTTTCTATTG	ATTGTGACAA	AATAAACTTA	2760
TTCCGTGGTG	TCTTTGCGTT	TCTTTTATAT	GTTGCCACCT	TTATGTATGT	ATTTTCTACG	2820
TTTGCTAACA	TACTGCGTAA	TAAGGAGTCT	TAATCATGCC	AGTTCTTTTG	GGTATTCCGT	2880
TATTATTGCG	TTTCCTCGGT	TTCCTTCTGG	TAACTTTGTT	CGGCTATCTG	CTTACTTTTC	2940
TTAAAAGGG	CTTCGGTAAG	ATAGCTATTG	CTATTTTCATT	GTTTCTTGCT	CTTATTATTG	3000
GGCTTAACTC	AATTCTTG TG	GGTTATCTCT	CTGATATTAG	CGCTCAATTA	CCCTCTGACT	3060
TTGTTCAAGG	TGTTCAAGTA	ATTCTCCCGT	CTAATGCGCT	TCCCTGTTTT	TATGTTATTC	3120
TCTCTGTAAA	GGCTGCTATT	TTCATTTTTG	ACGTAAACA	AAAAATCGTT	TCTTATTTGG	3180
ATTGGGATAA	ATAATATGGC	TGTTTATTTT	GTAAGTGGCA	AATTAGGCTC	TGGAAAGACG	3240
CTCGTTAGCG	TTGGTAAGAT	TTAGGATAAA	ATTGTAGCTG	GGTGCAAAAT	AGCAACTAAT	3300
CTTGATTAA	GGCTTCAAAA	CCTCCCGCAA	GTGCGGAGGT	TCGCTAAAC	GCCTCGCGTT	3360
CTTAGAATAC	CGGATAAGCC	TTCTATATCT	GATTTGCTTG	CTATTGGGCG	CGGTAATGAT	3420
TCCTACGATG	AAAATAAAAA	CGGCTTGCTT	GTTCTCGATG	AGTGCGGTAC	TTGGTTTAAAT	3480
ACCCGTTCTT	GGAATGATAA	GGAAAGACAG	CCGATTATTG	ATTGGTTTCT	ACATGCTCGT	3540
AAATTAGGAT	GGGATATTAT	TTTTCTTGTT	CAGGACTTAT	CTATTGTTGA	TAAACAGGCG	3600
CGTTCTGCAT	TAGCTGAACA	TGTTGTTTAT	TGTCGTCGTC	TGGACAGAAT	TACTTTACCT	3660
TTTGTGCGTA	CTTTATATTC	TCTTATTACT	GGCTCGAAAA	TGCCTCTGCC	TAAATTACAT	3720
GTTGGCGTTG	TTAAATATGG	CGATTCTCAA	TTAAGCCCTA	CTGTTGAGCG	TTGGCTTTAT	3780
ACTGGTAAGA	ATTTGTATAA	CGCATATGAT	ACTAAACAGG	CTTTTCTAG	TAATTATGAT	3840
TCCGGTGTTT	ATTCTTATTT	AACGCCTTAT	TTATCACACG	GTGCGTATTT	CAAACCATTA	3900
AATTTAGGTC	AGAAGATGAA	GCTTACTAAA	ATATATTTGA	AAAAGTTTTT	ACGCGTTCTT	3960
TGTCTTGCGA	TTGGATTGTC	ATCAGCATT	ACATATAGTT	ATATAACCCA	ACCTAAGCCG	4020
GAGGTTAAAA	AGGTAGTCTC	TCAGACCTAT	GATTTTGATA	AATTCACAT	TGACTCTTCT	4080
CAGCGTCTTA	ATCTAAGCTA	TCGCTATGTT	TTCAAGGATT	CTAAGGGAAA	ATTAATTAAT	4140
AGCGACGATT	TACAGAAGCA	AGGTTATTCA	CTCACATATA	TTGATTTATG	TACTGTTTCC	4200

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ATTAAAAAAG	GTAATTCAAA	TGAAATTGTT	AAATGTAATT	AATTTTGTTT	TCTTGATGTT	4260
TGTTTCATCA	TCTTCTTTTG	CTCAGGTAAT	TGAAATGAAT	AATTCGCCTC	TGCGCGATTT	4320
TGTAACCTGG	TATTCAAAGC	AATCAGGCGA	ATCCGTTATT	GTTTCTCCCG	ATGTAAAAGG	4380
TACTGTTACT	GTATATTCAT	CTGACGTTAA	ACCTGAAAAT	CTACGCAATT	TCTTTATTTT	4440
TGTTTTACGT	GCTAATAATT	TTGATATGGT	TGGTTCAATT	CCTTCCATAA	TTCAGAAGTA	4500
TAATCCAAAC	AATCAGGATT	ATATTGATGA	ATTGCCATCA	TCTGATAATC	AGGAATATGA	4560
TGATAATTCC	GCTCCTTCTG	GTGGTTTCTT	TGTTCCGCAA	AATGATAATG	TTACTCAAAC	4620
TTTTAAAATT	AATAACGTTT	GGGCAAAGGA	TTTAATACGA	GTTGTCGAAT	TGTTTGTAAG	4680
GTCTAATACT	TCTAAATCCT	CAAATGTATT	ATCTATTGAC	GGCTCTAATC	TATTAGTTGT	4740
TAGTGCACCT	AAAGATATTT	TAGATAACCT	TCCTCAATTC	CTTTCTACTG	TTGATTTGCC	4800
AACTGACCAG	ATATTGATTG	AGGGTTTGAT	ATTTGAGGTT	CAGCAAGGTG	ATGCTTTAGA	4860
TTTTTCATTT	GCTGCTGGCT	CTCAGCGTGG	CACTGTTGCA	GGCGGTGTTA	ATACTGACCG	4920
CCTCACCTCT	GTTTTATCTT	CTGCTGGTGG	TTCGTTGCGT	ATTTTAAATG	GCGATGTTTT	4980
AGGGCTATCA	GTTTCGCGCAT	TAAAGACTAA	TAGCCATTCA	AAAATATTGT	CTGTGCCACG	5040
TATTCTTACG	CTTTCAGGTC	AGAAGGGTTC	TATCTCTGTT	GGCCAGAATG	TCCCTTTTAT	5100
TACTGGTCGT	GTGACTGGTG	AATCTGCCAA	TGTAAATAAT	CCATTTTCAGA	CGATTGAGCG	5160
TCAAAATGTA	GGTATTTCCA	TGAGCGTTTT	TCCTGTTGCA	ATGGCTGGCG	GTAATATTGT	5220
TCTGGATATT	ACCAGCAAGG	CCGATAGTTT	GAGTTCTTCT	ACTCAGGCAA	GTGATGTTAT	5280
TACTAATCAA	AGAAGTATTG	CTACAACGGT	TAATTTGCGT	GATGGACAGA	CTCTTTTACT	5340
CGGTGGCCTC	ACTGATTATA	AAAACACTTC	TCAAGATTCT	GGCGTACCGT	TCCTGTCTAA	5400
AATCCCTTTA	ATCGGCCTCC	TGTTTAGCTC	CCGCTCTGAT	TCCAACGAGG	AAAGCACGTT	5460
ATACGTGCTC	GTCAAAGCAA	CCATAGTACG	CGCCCTGTAG	CGGCGCATTA	AGCGCGGCGG	5520
GTGTGGTGGT	TACGCGCAGC	GTGACCGCTA	CACTTGCCAG	CGCCCTAGCG	CCCCTCCTT	5580
TCGCTTTCTT	CCCTTCCTTT	CTCGCCACGT	TCGCCGGCTT	TCCCCGTCAA	GCTCTAAATC	5640
GGGGGCTCCC	TTTAGGGTTC	CGATTTAGTG	CTTTACGGCA	CCTCGACCCC	AAAAAATTG	5700
ATTTGGGTGA	TGGTTCACGT	AGTGGGCCAT	CGCCCTGATA	GACGGTTTTT	CGCCCTTTGA	5760
CGTTGGAGTC	CACGTTCTTT	AATAGTGGAC	TCTTGTTCCA	AACTGGAACA	AACTCAACC	5820
CTATCTCGGG	CTATTCTTTT	GATTTATAAG	GGATTTTGCC	GATTTTCGGAA	CCACCATCAA	5880
ACAGGATTTT	CGCCTGCTGG	GGCAAACCAG	CGTGGACCGC	TTGCTGCAAC	TCTCTCAGGG	5940
CCAGGCGGTG	AAGGGCAATC	AGCTGTTGCC	CGTCTCGCTG	GTGAAAAGAA	AAACCACCCT	6000
GGCGCCCAAT	ACGCAAACCG	CCTCTCCCCG	CGCGTTGGCC	GATTCATTAA	TGCAGCTGGC	6060
ACGACAGGTT	TCCCGACTGG	AAAGCGGGCA	GTGAGCGCAA	CGCAATTAAT	GTGAGTTAGC	6120
TCACTCATT	GGCACCCAG	GCTTTACACT	TTATGCTTCC	GGCTCGTATG	TTGTGTGGAA	6180
TTGTGAGCGG	ATAACAATTT	CACACGCGTC	ACTTGGCACT	GGCCGTCGTT	TTACAACGTC	6240

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GTGACTGGGA AAACCCTGGC GTTACCCAAG CTTTGTACAT GGAGAAAATA AAGTGAAACA	6300
AAGCACTATT GCACTGGCAC TCTTACCGTT ACTGTTTACC CCTGTGGCAA AAGCCCTTCT	6360
GAGGCATCCG GGAGCTGAAG GCGATGACCC TGCTAAGGCT GCATTCAATA GTTTACAGGC	6420
AAGTGCTACT GAGTACATTG GCTACGCTTG GGCTATGGTA GTAGTTATAG TTGGTGCTAC	6480
CATAGGGATT AAATTATTCA AAAAGTTTAC GAGCAAGGCT TCTTAAGCAA TAGCGAAGAG	6540
GCCCCGACCG ATCGCCCTTC CCAACAGTTG CGCAGCCTGA ATGGCGAATG GCGCTTTGCC	6600
TGGTTTCCGG CACCAGAAGC GGTGCCGAA AGCTGGCTGG AGTGCGATCT TCCTGAGGCC	6660
GATACGGTCG TCGTCCCCTC AAACCTGGCAG ATGCACGGTT ACGATGCGCC CATCTACACC	6720
AACGTAACCT ATCCCATTAC GGTCAATCCG CCGTTTGTTT CCACGGAGAA TCCGACGGGT	6780
TGTTACTCGC TCACATTTAA TGGTGATGAA AGCTGGCTAC AGGAAGGCCA GACGCGAATT	6840
ATTTTTGATG GCGTTCCTAT TGGTTAAAAA ATGAGCTGAT TTAACAAAAA TTTAACGCGA	6900
ATTTTAACAA AATATTAACG TTTACAATTT AAATATTTGC TTATACAATC TTCCTGTTTT	6960
TGGGGCTTTT CTGATTATCA ACCGGGGTAC ATATGATTGA CATGCTAGTT TTACGATTAC	7020
CGTTCATCGA TTCTCTTGTT TGCTCCAGAC TCTCAGGCAA TGACCTGATA GCCTTTGTAG	7080
ATCTCTCAA AATAGCTACC CTCTCCGGCA TTAATTTATC AGCTAGAACG GTTGAATATC	7140
ATATTGATGG TGATTGACT GTCTCCGGCC TTTCTCACC TTTTGAATCT TTACCTACAC	7200
ATTACTCAGG CATTGCATTT AAAATATATG AGGGTTCTAA AAATTTTTAT CCTTGCGTTG	7260
AAATAAAGGC TTCTCCCGCA AAAGTATTAC AGGGTCATAA TGTTTTTGGT ACAACCGATT	7320
TAGCTTTATG CTCTGAGGCT TTATTGCTTA ATTTTGCTAA TTCTTTGCCT TGCCTGTATG	7380
ATTTATTGGA CGTT	7394

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GATCCTAGGC TGAAGGCGAT GACCCTGCTA AGGCTGC

37

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATTCAATAGT TTACAGGCAA GTGCTACTGA GTACA

35

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(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTGGCTACGC TTGGGCTATG GTAGTAGTTA TAGTT

35

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGTGCTACCA TAGGGATTAA ATTATTCAA AAGTT

35

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TACGAGCAAG GCTTCTTA

18

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGCTTAAGAA GCCTTGCTCG TAACTTTTT GAATAATTT

39

103

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AATCCCTATG GTAGCACCAA CTATAACTAC TACCAT

36

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGCCCAAGCG TAGCCAATGT ACTCAGTAGC ACTTG

35

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCTGTAAACT ATTGAATGCA GCCTTAGCAG GGTC

34

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATCGCCTTCA GCCTAG

16

104

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 bas pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTCGAATTTCG TACATCCTGG TCATAGC

27

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CATTTTTGCA GATGGCTTAG A

21

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TAGCATTAAAC GTCCAATA

18

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATATATTTTA GTAAGCTTCA TCTTCT

26

105

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GACAAAGAAC GCGTGAAAAC TTT

23

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCGGGCCTCT TCGCTATTGC TTAAGAAGCC TTGCT

35

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TTCAGCCTAG GATCCGCCGA GCTCTCCTAC CTGCGAATTC GTACATCC

48

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGGATTATAC TTCTAAATAA TGGA

24

106

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TAACACTCAT TCCGGATGGA ATTCTGGAGT CTGGGT

36

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AATTCGCCAA GGAGACAGTC AT

22

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AATGAAATAC CTATTGCCTA CGGCAGCCGC TGGATTGTT

39

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATTACTCGCT GCCCAACCAG CCATGGCCGA GCTCGTGAT

39

107

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GACCCAGACT CCAGATATCC AACAGGAATG AGTGTTAAT

39

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TCTAGAACGC GTC

13

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ACGTGACGCG TTCTAGAATT AACACTCATT CCTGT

35

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TGGATATCTG GACTCTGGGT CATCAGAGC TCGGCCATG

39

108

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GCTGGTTGGG CAGCGAGTAA TAACAATCCA GCGGCTGCC

39

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GTAGGCAATA GGTATTTTCAT TATGACTGTC CTTGGCG

37

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TGACTGTCTC CTTGGCGTGT GAAATTGTTA

30

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TAACACTCAT TCCGGATGGA ATTCTGGAGT CTGGGT

36

109

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CAATTTTATC CTAAATCTTA CCAAC

25

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CATTTTTCGA GATGGCTTAG A

21.25

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CGAAAGGGGG GTGTGCTGCA A

21.25

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TAGCATTAAC GTCCAATA

18

110

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AAACGACGGC CAGTGCCAAG TGACGCGTGT GAAATTGTTA TCC

43

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GGCGAAAGGG AATTCTGCAA GGCGATTAAG CTTGGGTAAC GCC

43

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GGCGTTACCC AAGCTTTGTA CATGGAGAAA ATAAAG

36

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TGAAACAAAG CACTATTGCA CTGGCACTCT TACCGTTACC GT

42

111

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TACTGTTTAC CCCTGTGACA AAAGCCGCCC AGGTCCAGCT GC

42

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TCGAGTCAGG CCTATTGTGC CCAGGGATTG TACTAGTGGA TCCG

44

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TGGCGAAAGG GAATTCGGAT CCACTAGTAC AATCCCTG

38

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GGCACAATAG GCCTGACTCG AGCAGCTGGA CCAGGGCGGC TT

42

112

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TTGTCACAGG GGTAACAGT AACGGTAACG GTAAGTGTGC CA 42

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTGCAATAGT GCTTTGTTTC ACTTTATTTT CTCCATGTAC AA 42

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TAACGGTAAG AGTGCCAGTG C 21

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc_difference
- (B) LOCATION: replace(25, "")
- (D) OTHER INFORMATION: /note= ""M represents an equal mixture of A and C at this location and at locations 28, 31, 34, 37, 40, 43, 46 & 49""

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

AGCTCCCGGA TGCCTCAGAA GATGMNNMNN MNNMNNMNNM NNMNNMNNMN NGGCTTTTGC 60

CACAGGGG 68

113

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc_difference
(B) LOCATION: replace(17, "")
(D) OTHER INFORMATION: /note= ""M represents an equal mixture of A and C at this location and at locations 20, 23, 26, 29, 32, 35, 38, 41, 44 &

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CAGCCTCGGA TCCGCCMNNM NNMNNMNNMN NMNNMNNMNN MNNMNNATGM GAAT

54

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GGTAAACAGT AACGGTAAGA GTGCCAG

27

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GGGCTTTTGC CACAGGGGT

19

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

AGGGTCATCG CCTTCAGCTC CGGATCCCTC AGAAGTCATA AACCCCCCAT AGGCTTTTGC

60

CAC

63

114

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TCGCCTTCAG CTCCCGGATG CCTCAGAAGC ATGAACCCCC CATAGGC

47

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CAATTTTATC CTAAATCTTA CCAAC

25

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCCTTCAGCC TCGGATCCGC C

21

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CGGATGCCTC AGAAGCCCCN N

21

115

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 bas pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CGGATGCCTC AGAAGGGCTT TTGCCACAGG

30

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Thr	Gln	Ser	Lys	Cys	Ser	Thr	Asp	His	Trp	Leu	Gly	Tyr	Ile	Glu	Tyr
1				5					10					15	
Phe Ile Met Cys Thr Tyr															
20															

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Cys	Asp	Asp	Gln	Tyr	Tyr	Thr	Asp	His	Glu	Gln	Gly	Lys	Cys	Glu	Val
1				5					10					15	
Ala Leu Tyr Tyr Thr Gly															
20															

116

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Thr Gln Ser Lys Cys Ser Thr Asp His Trp Leu Gly Tyr Ile Glu Tyr
1 5 10 15
Phe Ile Met Cys Thr Tyr Arg Arg
 20

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Thr Cys Leu Arg Glu Glu Phe Ile Leu Gln Cys Tyr Ile Val Met Il
1 5 10 15
Glu Asp Trp Tyr
 20

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Ile Cys Glu His His Gln Met Leu Leu Gln Cys Ser Leu Val Cys Glu
1 5 10 15
Glu Cys Met Met
 20

117

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Lys Cys Ile Ile Gly Trp Tyr Thr Leu Thr Cys Tyr Met Ser Asp Arg
1 5 10 15
Pro Arg Met Glu
20

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Ala Cys Thr Gln Asp Met Asn Trp Ile Thr Cys Pro Met Tyr Cys Glu
1 5 10 15
Val Leu Cys Phe
20

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Val Cys Phe Tyr Phe Pro Phe Lys Met Met Cys His Met Glu Tyr Ile
1 5 10 15
Ala Tyr Glu Tyr
20

118

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Asp Ala Asn Cys Gly His Cys Thr Tyr Met Cys Ile Cys Lys Ile Met
1 5 10 15
Tyr Tyr Ile Ser
20

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Trp His Arg His Val Ser Ser Pro Met Ser Cys Trp Trp Tyr Asp Gln
1 5 10 15
Cys Ala Val Ala
20

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Cys Val Gln Ile Asp Phe Phe Thr Val Gln Cys Asn Ile Ser Ser His
1 5 10 15
Met Phe Leu Pro
20

I CLAIM:

1. A composition of matter comprising a plurality of cells containing a diverse population of expressible oligonucleotides, each of said oligonucleotides encoding a soluble peptide having
5 constrained secondary structure in solution, wherein each of said oligonucleotides is operationally linked to expression elements, said expressible oligonucleotides having a desirable bias of random codon sequences.

2. The composition of claim 1, wherein said oligonucleotides have more than one codon encoding an amino acid capable of forming a covalent bond.

3. The composition of claim 2, wherein said amino acid is an amino acid selected from the group consisting of cysteine, glutamic acid, lysine, leucine or tyrosine.

4. The composition of claim 2, wherein said oligonucleotide is selected from the group consisting of
TCLREEFILQCYIVMIEDWY, ICEHHQMLLQCSLVCEECEMM,
KCIIGWYTLTCYMSDRPRME, ACTQDMNWITCPMYCEVLCF,
VCFYFPFKMMCHMEYIAYEY, DANCGHCTYMCICKIMYYIS,
WERHVSSPMSCWWYDQCAVA and CVQIDFFTVCNIISSHMFLP

5. The composition of claim 1, wherein said cells are procaryotes.

6. The composition of claim 4, wherein said procaryotic cells are E. coli.

7. The composition of claim 1, wherein said expressible oligonucleotides are expressed as peptide fusion proteins on the surface of a filamentous bacteriophage.

8. A composition of matter comprising a plurality of cells containing a diverse population of expressible oligonucleotides, each of said oligonucleotides encoding a soluble peptide having
5 constrained secondary structure in solution, wherein each of said oligonucleotides is operationally linked to expression elements, said expressible oligonucleotides having a desirable bias of random codon sequences produced from random combinations of first and second
10 oligonucleotide precursor populations, each or either of said first and second precursor having a desirable bias of random codon sequences.

9. The composition of claim 8, wherein said first or second precursor oligonucleotides are biased.

10. The composition of claim 8, wherein said first and second precursor oligonucleotides are biased.

11. The composition of claim 8, wherein said first or second precursor oligonucleotides have more than one codon encoding an amino acid capable of forming a covalent bond.

12. The composition of claim 8, wherein said first and second precursor oligonucleotides have at least one codon encoding an amino acid capable of forming a covalent bond.

13. The composition of claim 8, wherein said oligonucleotide is selected from the group consisting of
TCLREEFILQCYIVMIEDWY, ICEHHQMLLQCSLVCEECEMM,
KCIIGWYTLTCYMSDRPRME, ACTQDMNWITCPMYCEVLCF,
VCFYFPFKMMCHMEYIAYEY, DANC GHCTYMCICKIMYYIS,
WREHVSSPMSCWWYDQCAVA and CVQIDFFT VQCNIS SHMFLP

14. The composition of claim 11 or 12, wherein said amino acid is an amino acid selected from the group consisting of cysteine, glutamic acid, lysine, leucine or tyrosine.

15. The composition of claim 8, wherein said cells are procaryotes.

16. The composition of claim 15, wherein said procaryotic cells are E. coli.

17. The composition of claim 8, wherein said expressible oligonucleotides are expressed as peptide fusion proteins on the surface of a filamentous bacteriophage.

18. A kit for the preparation of vectors useful for the expression of a diverse population of random soluble peptides having constrained secondary structure in solution, said peptides being generated from
5 combined first and second precursor oligonucleotides when combined having a desirable bias of random codon sequences, comprising: two vectors: a first vector having a cloning site for said first precursor oligonucleotides and a pair of restriction sites for operationally
10 combining first precursor oligonucleotides with second precursor oligonucleotides; and a second vector having a cloning site for said second precursor oligonucleotides and a pair of restriction sites complementary to those on said first vector, one or both vectors containing
15 expression elements capable of being operationally linked to said combined first and second precursor oligonucleotides.

19. The kit of claim 18, wherein said vectors are in a filamentous bacteriophage.

20. The kit of claim 18, wherein said filamentous bacteriophage are M13.

21. The kit of claim 18, wherein said vectors are plasmids or phagemids.

22. The kit of claim 18, wherein said first or second precursor oligonucleotides are biased toward a pre-determined sequence.

23. The kit of claim 18, wherein said first and second precursor oligonucleotides are biased toward a predetermined sequence.

24. The kit of claim 18, wherein said first or second precursor oligonucleotides have more than one codon encoding an amino acid capable of forming a covalent bond.

25. The kit of claim 18, wherein said first and second precursor oligonucleotides have at least one codon encoding an amino acid capable of forming a covalent bond.

26. The kit of claim 24 or 25, wherein said amino acid is an amino acid selected from the group consisting of cysteine, glutamic acid, lysine, leucine or tyrosine.

27. A cloning system for expressing
oligonucleotides encoding random, soluble peptides having
constrained secondary structure in solution, said
oligonucleotides being generated from a desirable bias of
5 random codon sequences, comprising a vector having a pair
of restriction sites so as to allow the operational
combination of said oligonucleotides into a contiguous
oligonucleotide encoding said soluble peptide having
constrained secondary structure in solution.

28. The cloning system of claim 27, wherein
said oligonucleotides have more than one codon encoding
an amino acid capable of forming a covalent bond.

29. A cloning system for expressing oligonucleotides encoding random, soluble peptides having constrained secondary structure in solution, said oligonucleotides being generated from diverse populations
5 of combined first and second precursor oligonucleotides each or either having a desirable bias of random codon sequences, comprising: a set of first vectors having a desirable bias of random codon sequences and a second set of vectors having a diverse population of second
10 precursor oligonucleotides having a desirable bias of random codon sequences, said first and second vectors each having a pair of restriction sites so as to allow the operational combination of said oligonucleotides into a contiguous oligonucleotide encoding said soluble
15 peptide having constrained secondary structure in solution.

30. The composition of claim 29, wherein said first or second precursor oligonucleotides are biased.

31. The composition of claim 29, wherein said first and second precursor oligonucleotides are biased.

32. The cloning system of claim 29, wherein said first or second precursor oligonucleotides have more than one codon encoding an amino acid capable of forming a covalent bond.

33. The cloning system of claim 29, wherein said first and second precursor oligonucleotides have at least one codon encoding an amino acid capable of forming a covalent bond.

34. The cloning system of claim 32 or 33, wherein said amino acid is an amino acid selected from the group consisting of cysteine, glutamic acid, lysine, leucine or tyrosine.

35. The cloning system of claim 29, wherein said combined first and second vectors is through a pair of restriction sites.

36. The cloning system of claim 29, wherein said expressible oligonucleotides are expressed as peptide fusion proteins on the surface of a filamentous bacteriophage.

37. A vector comprising an oligonucleotide, said oligonucleotide having a desirable bias of random codon sequences, and more than one codon encoding an amino acid capable of forming a covalent bond.

38. A vector of claim 37, wherein said amino acid is an amino acid selected from the group consisting of cysteine, glutamic acid, lysine, leucine or tyrosine.

39. An isolated, soluble peptide having a constrained secondary structure in solution.

40. An expressible oligonucleotide produced by the cloning system of claim 29.

41. A host cell containing the cloning system of claim 29.

42. A host cell containing the vector of claim 38.

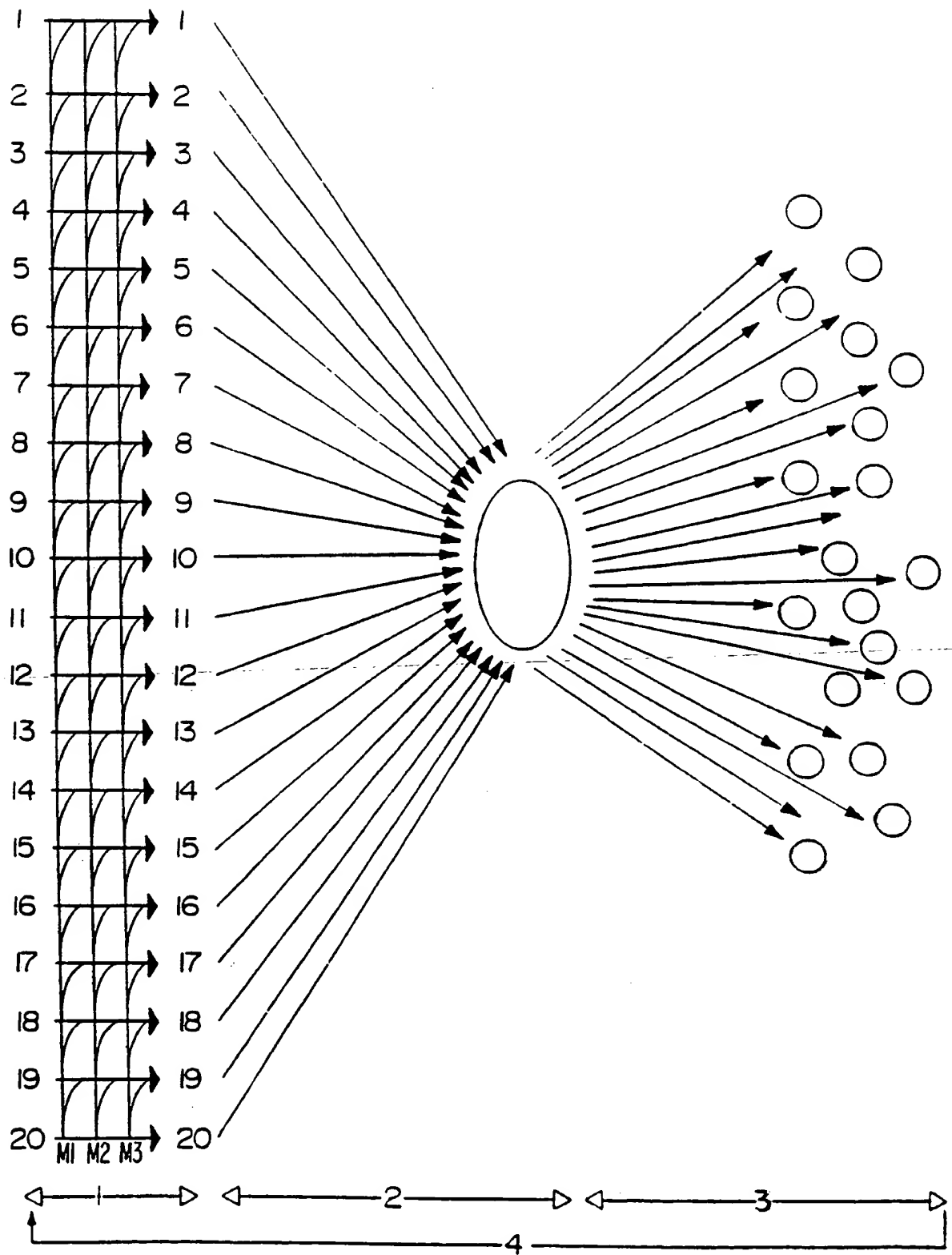
43. A method of isolating a soluble peptide having a constrained secondary structure in solution, which comprises growing said host cell of claim 41 or 42 under suitable conditions favoring expression of said peptide, and isolating said peptide so produced.

44. A method of constructing a diverse population of vectors containing combined first and second precursor oligonucleotides, wherein each or either precursor oligonucleotides has a desirable bias of random codon sequences, and capable of expressing said combined oligonucleotides as random, soluble peptides having constrained secondary structure in solution, comprising the steps of:

- 5 (a) operationally linking sequences from a diverse population of first precursor oligonucleotides having a desirable bias of random codon sequences to a first vector;
- 10 (b) operationally linking sequences from a diverse population of second precursor oligonucleotides having a desirable bias of random codon sequences to a second vector;
- (c) wherein said first or second, or first and second precursor oligonucleotides have at least one codon capable of forming a covalent bond,
- 15 (d) combining the vector products of steps (a) and (b) under conditions where said populations of first and second precursor oligonucleotides are joined together into a population of combined vectors capable
- 20 of being expressed.

45. The method of claim 44, wherein said amino acid is an amino acid selected from the group consisting of cysteine, glutamic acid, lysine, leucine or tyrosine.

46. The method of claim 44, wherein steps (a) through (d) are repeated two or more times.



SUBSTITUTE SHEET

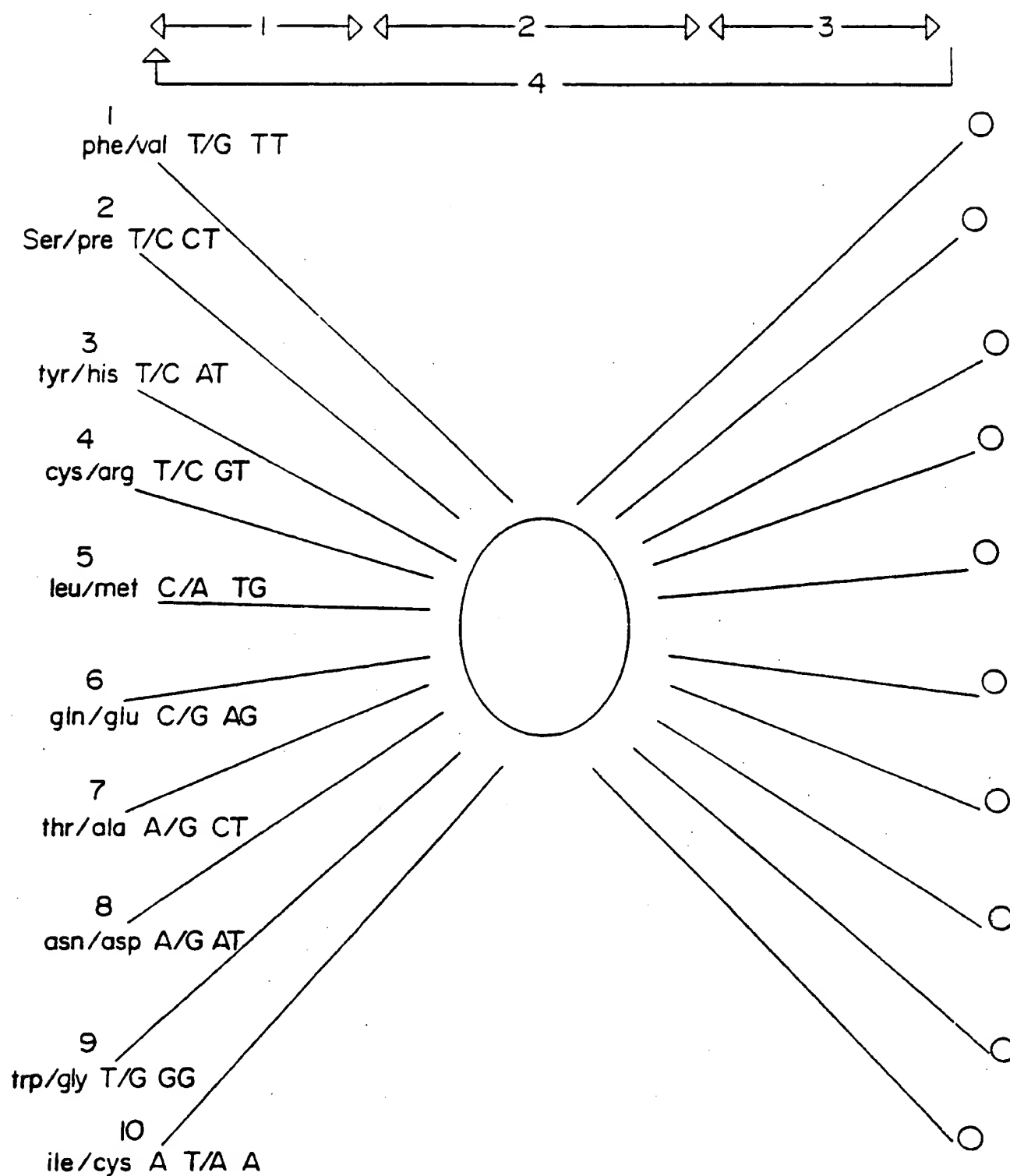
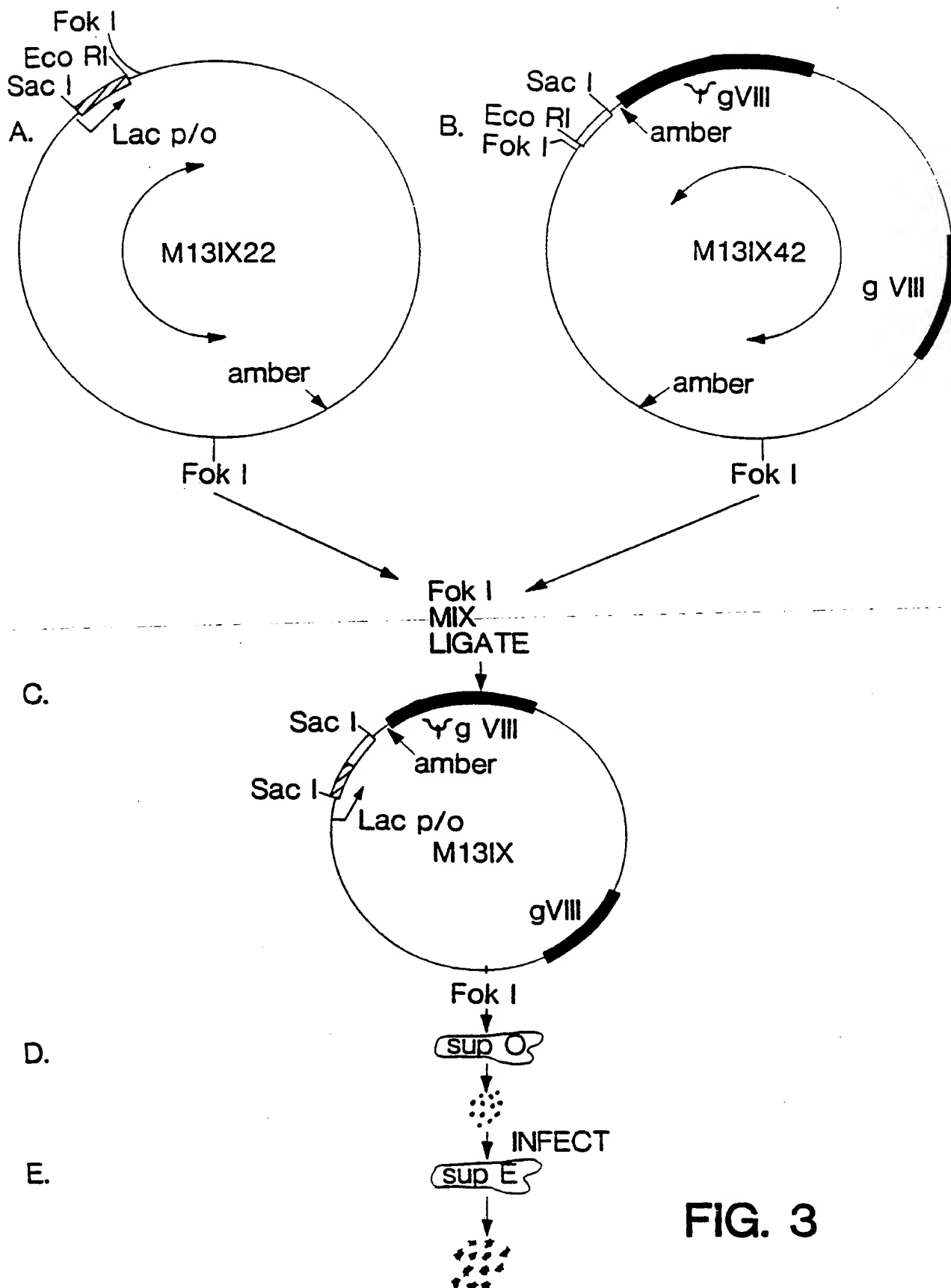


FIG. 2



SUBSTITUTE SHEET

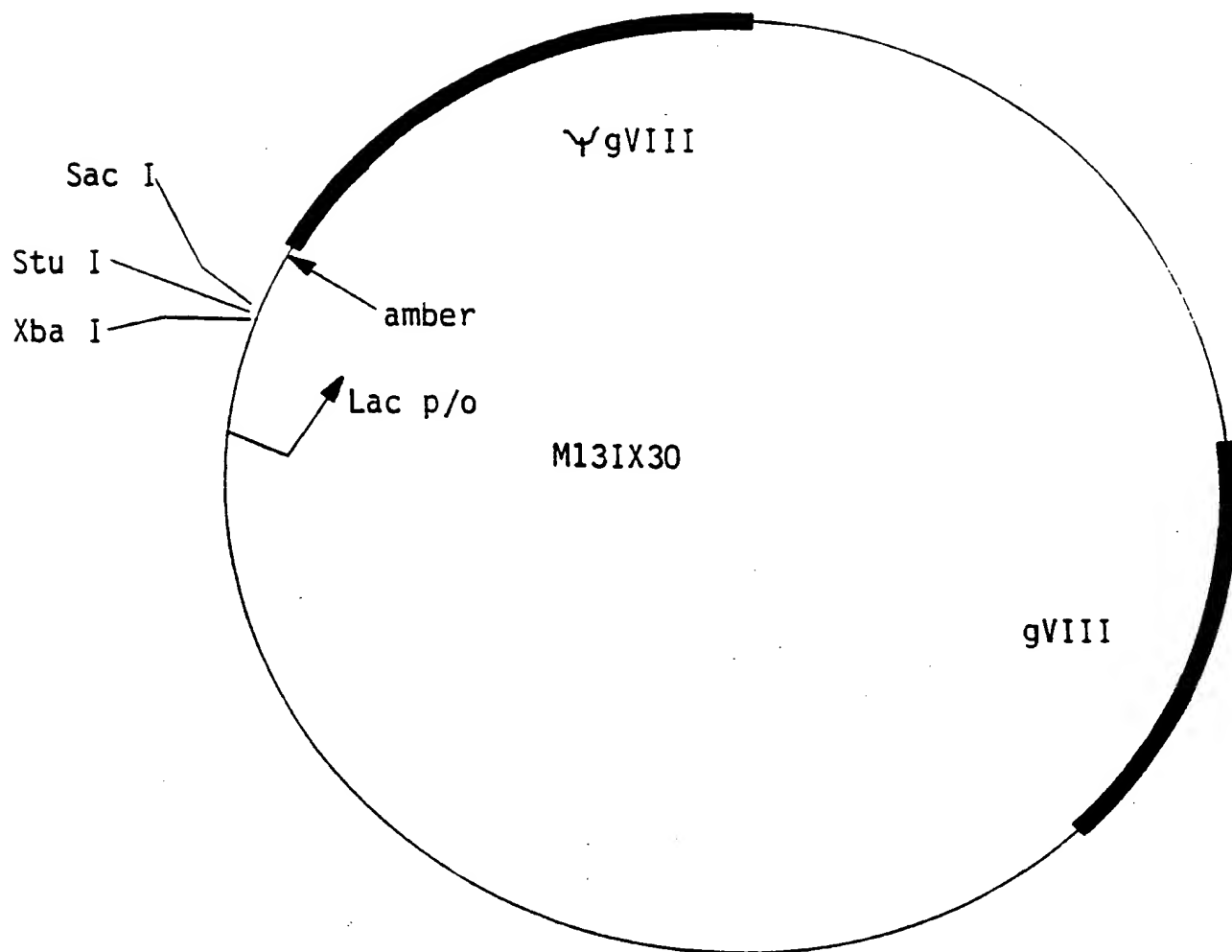


FIG. 4

1	AATGCTACTA	CTATTAGTAG	AATTGATGCC	ACCTTTTCAG	CTCGCGCCCC	AAATGAAAAT	60
61	ATAGCTAAAC	AGGTTATTGA	CCATTTGCGA	AATGTATCTA	ATGGTCAAAC	TAAATCTACT	120
121	CGTTTCGCAGA	ATTGGGAATC	AACTGTTACA	TGGAATGAAA	CTTCCAGACA	CCGTACTTTA	180
181	GTTGCAATAT	TAAAACATGT	TGAGCTACAG	CACCAGATTC	AGCAATTAAG	CTCTAAGCCA	240
241	TCTGCAAAAA	TGACCTCTTA	TCAAAAGGAG	CAATTAAAGG	TACTCTCTAA	TCCTGACCTG	300
301	TTGGAGTTTG	CTTCCGGTCT	GGTTCGCTTT	GAAGCTCGAA	TTAAACGCG	ATATTTGAAG	360
361	TCTTTCGGGC	TTCTCTTAA	TCTTTTGTAT	GCAATCCGCT	TTGCTTCTGA	CTATAATAGT	420
421	CAGGGTAAAG	ACCTGATTTT	TGATTTATGG	TCATTCTCGT	TTTCTGAACT	GTTTAAAGCA	480
481	TTTGAGGGGG	ATTCAATGAA	TATTTATGAC	GATTCCGCG	TATTGGACGC	TATCCAGTCT	540
541	AAACATTTTA	CTATTACCCC	CTCTGGCAAA	ACTTCTTTTG	CAAAAGCCTC	TCGCTATTTT	600
601	GGTTTTTATC	GTCGTCTGGT	AAACGAGGGT	TATGATAGTG	TTGCTCTTAC	TATGCCTCGT	660
661	AATTCCTTTT	GGCGTTATGT	ATCTGCATTA	GTTGAATGTG	GTATTCCTAA	ATCTCAACTG	720
721	ATGAATCTTT	CTACCTGTAA	TAATGTTGTT	CCGTTAGTTC	GTTTTATTAA	CGTAGATTTT	780
781	TCTTCCCAAC	GTCCTGACTG	GTATAATTAG	CCAGTCTTAA	AAATCGCATA	AGGTAATTTA	840
841	CAATGATTAA	AGTTGAAATT	AAACCATCTC	AAGCCCAATT	TACTACTCGT	TCTGGTGTGT	900
901	CTCGTCAGGG	CAAGCCTTAT	TCACTGAATG	AGCAGCTTTG	TTACGTTGAT	TTGGGTAATG	960
961	AATATCCGGT	TCTTGTCAAG	ATTACTCTTG	ATGAAGGTCA	GCCAGCCTAT	GCGCCTGGTC	1020
1021	TGTACACCGT	TCATCTGTCC	TCTTTCAAAG	TTGGTCAAGT	CGGTTCCCTT	ATGATTGACC	1080
1081	GTCTGCGCCT	CGTTCGGGCT	AAGTAACATG	GAGCAGGTG	CGGATTTCTGA	CACAAATTTT	1140
1141	CAGGCGATGA	TACAAATCTC	CGTTGTACTT	TGTTTCGCGC	TTGGTATAAT	CGCTGGGGGT	1200
1201	CAAAGATGAG	TGTTTTAGTG	TATTTCTTCG	CCTCTTTCGT	TTTAGGTTGG	TGCTTTCGTA	1260
1261	GTGGCATTAC	GTATTTTACC	CGTTTAATGG	AAACTTCCTC	ATGAAAAAGT	CTTTAGTCCT	1320
1321	CAAAGCCTCT	GTAGCCGTTG	CTACCCTCGT	TCCGATGCTG	TCTTTCGCTG	CTGAGGGTGA	1380
1381	CGATCCCGCA	AAAGCGGCCT	TTAACTCCCT	GCAAGCCTCA	GCGACCGAAT	ATATCGGTTA	1440
1441	TGCGTGGGCG	ATGGTTGTTG	TCATTGTGCG	CGCAACTATC	GGTATCAAGC	TGTTTAAAGAA	1500
1501	ATTCACCTCG	AAAGCAAGCT	GATAAACCGA	TACAATTAAT	GGCTCCTTTT	GGAGCCTTTT	1560
1561	TTTTTGGAGA	TTTTCAACGT	GAAAAAATTA	TTATTCGCAA	TTCTTTTAGT	TGTTCTTTTC	1620
1621	TATTTCTACT	CCGCTGAAAC	TGTTGAAAGT	TGTTTAGCAA	AAACCCATAC	AGAAAAATTCA	1680
1681	TTTACTAACG	TCTGGAAAGA	CGACAAAATC	TTAGATCGTT	ACGCTAACTA	TGAGGGTGTG	1740
1741	CTGTGGAATG	CTACAGGCGT	TGTAGTTTGT	ACTGGTGACG	AAACTCAGTG	TTACGGTACA	1800
1801	TGGGTTTCTA	TTGGGCTTGC	TATCCCTGAA	AATGAGGGTG	GTGGCTCTGA	GGGTGGCGGT	1860
1861	TCTGAGGGTG	GCGGTTCTGA	GGGTGGCGGT	ACTAAACCTC	CTGAGTACGG	TGATACACCT	1920
1921	ATTCCGGGCT	ATACTTATAT	CAACCCTCTC	GACGGCACTT	ATCCGGCTGG	TACTAGACAA	1980
1981	AACCCCGCTA	ATCTTAATCC	TTCTCTTGAG	GAGTCTCAGC	CTCTTAATAC	TTTCATGTTT	2040
2041	CAGAATAATA	GGTTCGGAAT	TAGGCAGGGG	GCATTAACCTG	TTTATACGGG	CACTGTTACT	2100
2101	CAAGGCACCTG	ACCCCGTTAA	AACCTTATAC	CAGTACACTC	CTGTATCATC	AAAAGCCATG	2160
2161	TATGACGCTT	ACTGGAACGG	TAAATTCAGA	GACTGCGCTT	TCCATTCTGG	CTTTAATGAA	2220
2221	GATCCATTCTG	TTTGTGAATA	TCAAGGCCAA	TCGTCTGACC	TCGGTCAACC	TCCTGTCAAT	2280
2281	GCTGGCGGCG	GCTCTGGTGG	TGGTTCTGGT	GGCGGCTCTG	AGGGTGGGTG	CTCTGAGGGT	2340
2341	GGCGGTTCTG	AGGGTGCGCG	CTCTGAGGGA	GGCGGTTCCG	GTGGTGCGTC	TGGTTCCGGT	2400
2401	GATTTTGAAT	ATGAAAAGAT	GGCAAACGCT	AATAAGGGGG	CTATGACCGA	AAATGCCGAT	2460
2461	GAAAACGCGC	TACAGTCTGA	CGCTAAAGGC	AAACTTGATT	CTGTCGCTAC	TGATTACGGT	2520
2521	GCTGCTATCG	ATGGTTTCAT	TGGTGAGGTT	TCCGGCCTTG	CTAATGGTAA	TGGTGCTACT	2580
2581	GGTGATTTTG	CTGGCTCTAA	TTCCCAAATG	GCTCAAGTCTG	GTGACGGTGA	TAAATCACTT	2640
2641	TTAATGAATA	ATTTCCGTCA	ATATTTACCT	TCCCTCCCTC	AATCGGTTGA	ATGTCGCCCT	2700
2701	TTTGTCTTTA	GCGCTGGTAA	ACCATATGAA	TTTTCTATTG	ATTGTGACAA	AATAAACTTA	2760
2761	TTCCGTGGTG	TCTTTGCGTT	TCTTTTATAT	GTTGCCACCT	TTATGTATGT	ATTTTCTACG	2820
2821	TTTGCTAACCA	TACTGCGTAA	TAAGGAGTCT	TAATCATGCC	AGTTCTTTTG	GGTATTCGGT	2880
2881	TATTATTGCG	TTTCCTCGGT	TTCTTCTGGA	TAACCTTTGT	GCCGTATCTG	CTTACTTTTC	2940
2941	TTAAAAAGGG	CTTCGGTAAG	ATAGCTATTG	CTATTTTCATT	GTTTCTTGCT	CTTATTATTG	3000
3001	GGCTTAACTC	AATTCCTGTG	GGTTATCTCT	CTGATATTAG	CGCTCAATTA	CCCTCTGACT	3060
3061	TTGTTACAGG	TGTTCAAGTTA	ATTCTCCCGT	CTAATGCGCT	TCCCTGTTTT	TATGTTATTC	3120
3121	TCTCTGTAAA	GGCTGCTATT	TTCTTTTTTG	ACGTTAAACA	AAAAATCGTT	TCTTATTTGG	3180
3181	ATTGGGATAA	ATAATATGGC	TGTTTATTTT	GTAACCTGGCA	AATTAGGCTC	TGGAAAGACG	3240
3241	CTCGTTAGCG	TTGGTAAGAT	TCAGGATAAA	ATTGTAGACTG	GGTGCAAAAT	AGCAACTAAT	3300
3301	CCTGATTTAA	GGCTTCAAAA	CCTCCCGCAA	GTCGGGAGGT	TCGCTAAAAC	GCCCTCGGTT	3360
3361	CTTAGAATAC	CGGATAAGCC	TTCTATATCT	GATTTGCTTG	CTATTGGGCG	CGGTAATGAT	3420
3421	TCCTACGATG	AAAAATAAAA	CGGCTTGCTT	GTTCTCGATG	AGTGCGGTAC	TTGGTTTAAAT	3480
3481	ACCCGTTCTT	GGAATGATAA	GGAAAGACAG	CCGATTATTG	ATTGGTTTCT	ACATGCTCGT	3540
3541	AAATTAGGAT	GGGATATTAT	CTTCTTGTGT	CAGGACTTAT	CTATTGTTGA	TAAACAGGCG	3600
3601	CGTTCTGCAT	TAGCTGAACA	TCTTGTTTAT	TGTCGTCGTC	TGGACAGAAAT	TACTTTACCT	3660
3661	TTTGTGCGTA	CTTTATATTC	TCTTATTACT	GGCTCGAAAA	TGCCTCTGCC	TAAATTACAT	3720
3721	GTTGGCGTTG	TTAAATATGG	CGATTCTCAA	TTAAGCCCTA	CTGTTGAGCG	TTGGCTTTAT	3780
3781	ACTGGTAAGA	ATTTGTATAA	CGCATATGAT	ACTAAACAGG	CTTTTCTAG	TAATTATGAT	3840

FIG. 5-1

3841	TCCGGTGTTT	ATTCTTATTT	AACGCCTTAT	TTATCACACG	GTCGGTATTT	CAAACCATTA	3900
3901	AATTTAGGTC	AGAAGATGAA	GCTTACTAAA	ATATATTTGA	AAAAGTTTTT	ACGCGTTCTT	3960
3961	TGTCTTGCGA	TTGGATTTGC	ATCAGCATTT	ACATATAGTT	ATATAACCCA	ACCTAAGCCG	4020
4021	GAGGTAAAAA	AGGTAGTCTC	TCAGACCTAT	GATTTTGATA	AATTCACAT	TGACTCTTCT	4080
4081	CAGCGTCTTA	ATCTAAGCTA	TCGCTATGTT	TTCAAGGATT	CTAAGGGAAA	ATTAATTAAT	4140
4141	AGCGACGATT	TACAGAAGCA	AGGTTATTCA	CTCACATATA	TTGATTTATG	TACTGTTTCC	4200
4201	ATTA AAAAAGG	TAATTC AAAT	GAAATTGTTA	AATGTAATTA	ATTTTGTTTT	CTTGATGTTT	4260
4261	GTTTCATCAT	CTTCTTTTGC	TCAGGTAATT	GAAATGAATA	ATTCGCCTCT	GCGCGATTTT	4320
4321	GTAAC TTGGT	ATTCAAAGCA	ATCAGGCGAA	TCCGTTATTG	TTTCTCCCGA	TGTA AAAAGT	4380
4381	ACTGTTACTG	TATATT CATC	TGACGTTAAA	CCTGAAAATC	TACGCAATTT	CTTTATTTCT	4440
4441	GTTTTACGTG	CTAATAATTT	TGATATGGTT	GGTTCAATTC	CTTCCATTAT	TTAGAAGTAT	4500
4501	AATCCAAACA	ATCAGGATTA	TATTGATGAA	TTGCCATCAT	CTGATAATCA	GGAATATGAT	4560
4561	GATAATTTCCG	CTCCTTCTGG	TGGTTTCTTT	GTTCCGCAAA	ATGATAATGT	TACTCAAAC	4620
4621	TTTAAAATTA	ATAACGTTTG	GGCAAAGGAT	TTAATACGAG	TTGTCGAATT	GTTTGTAAG	4680
4681	TCTAATACTT	CTAAATCCTC	AAATGTATTA	TCTATTGACG	GCTCTAATCT	ATTAGTTGTT	4740
4741	AGTGACACCTA	AAGATATTTT	AGATAACCTT	CCTCAATTCC	TTTCTACTGT	TGATTTGCCA	4800
4801	ACTGACCAGA	TATTGATTGA	GGGTTTGATA	TTTGAGGTTT	AGCAAGGTGA	TGCTTTAGAT	4860
4861	TTTTCATTTG	CTGCTGGCTC	TCAGCGTGGC	ACTGTTGCAG	GCGGTGTTAA	TACTGACCGC	4920
4921	CTCACCTCTG	TTTTATCTTC	TGCTGGTGGT	TCGTTCCGTA	TTTTTAATGG	CGATGTTTTA	4980
4981	GGGCTATCAG	TTTCGCGCATT	AAAGACTAAT	AGCCATTCAA	AAATATTGTC	TGTGCCACGT	5040
5041	ATTCTTACGC	TTTCAGGTCA	GAAGGGTTCT	ATCTCTGTTG	GCCAGATAGT	CCCTTTTATT	5100
5101	ACTGGTCGTG	TGACTGGTGA	ATCTGCCAAT	GTAATAATC	CATTTCAGAG	CATTGAGCGT	5160
5161	CAAAATGTAG	GTATTTCCAT	GAGCGTTTTT	CCTGTTGCAA	TGGCTGGCGG	TAATATTGTT	5220
5221	CTGGATATTA	CCAGCAAGGC	CGATAGTTTG	AGTTCTTCTA	CTCAGGCAAG	TGATGTTATT	5280
5281	ACTAATCAAA	GAAGTATTGC	TACAACGGTT	AAATTTGCGT	ATGGACAGAC	TCTTTTACTC	5340
5341	GGTGCCCTCA	CTGATTATAA	AAACACTTCT	CAAGATTCTG	GCGTACCGTT	CCTGTCTAAA	5400
5401	ATCCCTTTAA	TCGGCCTCCT	GTTTAGCTCC	CGCTCTGATT	CCAACGAGGA	AAGCACGTTA	5460
5461	TACGTGCTCG	TCAAAGCAAC	CATAGTACGC	GCCCTGTAGC	GCGCGATTAA	GCGCGGCGGG	5520
5521	TGTGGTGGTT	ACGCGCAGCG	TGACCGCTAC	ACTTGCCAGC	GCCCTAGCGC	CCGCTCCTTT	5580
5581	CGTTTCTTTC	CCTTCTCTTC	TCGCCACGTT	CGCCGGCTTT	CCCCGTCAAG	CTCTAAATCG	5640
5641	GGGGCTCCCT	TTAGGGTTCC	GATTTAGTGC	TTTACGGCAC	CTCGACCCCA	AAAAACTTGA	5700
5701	TTTGGGTGAT	GGTTCACGTA	GTGGGCGCAT	GCCCTGTATG	ACGGTTTTTC	GCCCTTTGAC	5760
5761	GTTGGAGTCC	ACGTTCTTTA	ATAGTGGACT	CTTGTTCCAA	ACTGGAACAA	CACCTCAACC	5820
5821	TATCTCGGGC	TATTTCTTTT	ATTTATAAGG	GATTTTGCCG	ATTTGGAAC	CACCATCAAA	5880
5881	CAGGATTTTC	GCCTGCTGGG	GCAAACCAGC	GTGGACCGCT	TGCTGCAACT	CTCTCAGGGC	5940
5941	CAGGCGGTGA	AGGGCAATCA	GCTGTTGCC	GTCTCGCTGG	TGAAAAGAAA	AACCACCCTG	6000
6001	GCGCCCAATA	CGCAAACCGC	CTCTCCCGCG	GCGTTGGCCG	ATTCATTAAT	GCAGCTGGCA	6060
6061	CGACAGGTTT	CCCGACTGGA	AAGCGGGCAG	TAGAGCGAAC	GCAATTAATG	TGAGTTAGCT	6120
6121	CACTCATTAG	GCACCCAGG	CTTTACACTT	TATGCTTCCG	GCTCGTATGT	TGTTGTGAAT	6180
6181	TGTGAGCGGA	TAACAATTTT	ACACAGGAAA	CAGCTATGAC	CAGGATGTAC	GAATTGCGAG	6240
6241	GTAGGAGAGC	TCGGCGGATC	CTAGGCTGAA	GGCGATGACC	CTGCTAAGGC	TGCATTCAAT	6300
6301	AGTTTACAGG	CAAGTGCTAC	TGAGTACATT	GGCTACGCTT	GGGCTATGGT	AGTAGTTATA	6360
6361	GTTGGTGCTA	CCATAGGGAT	TAAATTATTC	AAAAAGTTTA	CGAGCAAGGC	TTCTTAACCA	6420
6421	GCTGGCGTAA	TAGCGAAGAG	GCCCGCACCG	ATCGCCCTTC	CCAACGATTG	CGCAGCCTGA	6480
6481	ATGGCGAATG	GCGCTTTGCC	TGGTTTCCGG	CACCAGAAGC	GGTGCCGGAA	AGCTGGCTGG	6540
6541	AGTGCGATCT	TCCTGAGGCC	GATACGGTCG	TCGTCCCTTC	AAACTGGCAG	ATGCACGGTT	6600
6601	ACGATGCGCC	CATCTACACC	AACGTAACCT	ATCCCATTA	GGTCAATCCG	CCGTTTGTTC	6660
6661	CCACGGAGAA	TCCGACGGGT	TGTTACTCGC	TCACATTTAA	TGTTGATGAA	AGCTGGCTAC	6720
6721	AGGAAGGCCA	GACGCGAATT	ATTTTGTAGT	CGGTTTCTAT	TGGTTAAAAA	ATGAGCTGAT	6780
6781	TTAACAAAAA	TTTAACGCGA	ATTTTAAACA	AATATTAACG	TTTACAATTT	AAATATTTGC	6840
6841	TTATACAATC	TTCTGTGTTT	TGGGGCTTTT	CTGATTATCA	ACCGGGGTAC	ATATGATTGA	6900
6901	CATGCTAGTT	TTACGATTAC	CGTTTCATCGA	TTCTCTTGTT	TGCTCCAGAC	TCTCAGGCAA	6960
6961	TGACCTGATA	GCCTTTGTAG	ATCTCTCAAA	AATAGCTACC	CTCTCCGGCA	TTAATTTATC	7020
7021	AGCTAGAACG	GTTGAATATC	ATATTGATGG	TGATTGTACT	GTCTCCGGCC	TTTCTCACCC	7080
7081	TTTTGAATCT	TTACCTACAC	ATTACTCAGG	CATTGCATTT	AAAAATATATG	AGGGTTCTAA	7140
7141	AAATTTTTTAT	CCTTGCGTTG	AAATAAAGGC	TTCTCCCGCA	AAAGTATTAC	AGGGTCATAA	7200
7201	TGTTTTTGGT	ACAACCGATT	TAGCTTTATG	CTCTGAGGCT	TTATTGCTTA	ATTTTGCTAA	7260
7261	TTCTTTGCCT	TGCCTGTATG	ATTTATTGGA	CGTT			7294
	10	20	30	40	50	60	

FIG. 5-2

1	AATGCTACTA	10	CTATTAGTAG	20	AATTGATGCC	30	ACCTTTTCAG	40	CTCGCGCCCC	50	AAATGAAAAT	60
61	ATAGCTAAAC	AGGTTATTGA	CCATTTGCGA	AATGTATCTA	ATGGTCAAAC	TAAATCTACT	120					
121	CGTTCCGAGA	ATTGGGAATC	AACTGTTACA	TGGAATGAAA	CTTCCAGACA	CCGTACTTTA	180					
181	GTTGCATATT	TAAAACATGT	TGAGCTACAG	CACCAGATTC	AGCAATTAAG	CTCTAAGCCA	240					
241	TCTGCAAAAA	TGACCTCTTA	TCAAAAGGAG	CAATTAAGG	TACTCTCTAA	TCCTGACCTG	300					
301	TTGGAGTTTG	CTTCCGGTCT	GGTTGCGTTT	GAAGCTCGAA	TTAAAACGCG	ATATTTGAAG	360					
361	TCTTTCGGGC	TTCCTCTTAA	TCTTTTTGAT	GCAATCCGCT	TTGCTTCTGA	CTATAATAGT	420					
421	CAGGGTAAAG	ACCTGATTTT	TGATTTATGG	TCATTCTCGT	TTTCTGAACT	GTTTAAAGCA	480					
481	TTTGAGGGGG	ATTCAATGAA	TATTTATGAC	GATTCCGCG	TATTGGACGC	TATCCAGTCT	540					
541	AAACATTTTA	CTATTACCCC	CTCTGGCAAA	ACTTCTTTTG	CAAAAGCCTC	TCGCTATTTT	600					
601	GGTTTTTATC	GTCGTCTGGT	AAACGAGGGT	TATGATAGTG	TTGCTCTTAC	TATGCCTCGT	660					
661	AATTCCTTTT	GGCGTTATGT	ATCTGCATTA	GTTGAATGTG	GTATTCCTAA	ATCTCAACTG	720					
721	ATGAATCTTT	CTACCTGTAA	TAATGTTGTT	CCGTTAGTTC	GTTTTATTAA	CGTAGATTTT	780					
781	TCTTCCCAAC	GTCCTGACTG	GTATAATGAG	CCAGTTCTTA	AAATCGCATA	AGGTAATTCA	840					
841	CAATGATTAA	AGTTGAAATT	AAACCATCTC	AAGCCCAATT	TACTACTCGT	TCTGGTGTGT	900					
901	CTCGTCAGGG	CAAGCCTTAT	TCACGTAAATG	AGCAGCTTTG	TTACGTTGAT	TTGGGTAAATG	960					
961	AATATCCGGT	TCTTGTCAAG	ATTACTCTTG	ATGAAGGTCA	GCCAGCCTAT	GCGCCTGGTC	1020					
1021	TGTACACCGT	TCATCTGTCC	TCTTTCAAAG	TTGGTCAGTT	CGGTTCCCTT	ATGATTGACC	1080					
1081	GTCTGCGCCT	CGTTCCGGCT	AAGTAACATG	GAGCAGGTCTG	CGGATTTCTGA	CACAATTTAT	1140					
1141	CAGGCGATGA	TACAAATCTC	CGTTGTACTT	TGTTTCGCGC	TTGGTATAAT	CGCTGGGGGT	1200					
1201	CAAGAGATTAG	TGTTTTAGTG	TATTTCTTTCG	CCTCTTTCTGT	TTTAGGTTGG	TGCCTTCGTA	1260					
1261	GTGGCATTAC	GTATTTTACC	CGTTTAAATG	AAACTTCTCTC	ATGAAAAAGT	CTTTAGTCTT	1320					
1321	CAAAGCCTCT	GTAGCCGTTG	CTACCCTCGT	TCCGATGCTG	TCTTTCGCTG	CTGAGGGTGA	1380					
1381	CGATCCCGCA	AAAGCGGCCT	TAACTCCCT	GCAAGCCTCA	GCGACCGAAT	ATATCGGTTA	1440					
1441	TGCGTGGGCG	ATGGTTGTTG	TCATTGTCTG	CGCAACTATC	GGTATCAAGC	TGTTTTAAGAA	1500					
1501	ATTCACCTCG	AAAGCAAGCT	GATAAACCGA	TACAATTAAT	GGCTCCTTTT	GGAGCCTTTT	1560					
1561	TTTTTGAGAA	TTTTCAACGT	GAAAAAATTA	TTATTCGCAA	TTCTTTTAGT	TGTTCTTTTC	1620					
1621	TATTTCTCACT	CCGCTGAAAC	TGTTGAAAGT	TGTTTAGCAA	AACCCCATAC	AGAAAATTCA	1680					
1681	TTTACTAACG	TCTGGAAAGA	CGACAAACT	TTAGATCGTT	ACGCTAACTA	TGAGGTTGT	1740					
1741	CTGTGGAATG	CTACAGGCGT	TGTAGTTTGT	ACTGGTGACG	AAACTCAGTG	TTACGGTACA	1800					
1801	TGGGTTCCCTA	TTGGGCTTGC	TATCCCTGAA	AATGAGGGTG	GTGGCTCTGA	GGGTGGCGGT	1860					
1861	TCTGAGGGTG	GCGGTTCTGA	GGGTGGCGGT	ACTAAACCTC	CTGAGTACGG	TGATACACCT	1920					
1921	ATTCCTGGCT	ATACCTATAT	CAACCTCTCT	GACGGCACTT	ATCCGCTGG	TACTGAGCAA	1980					
1981	AACCCCGCTA	ATCTTAATCC	TTCTCTTAGC	GAGTCTACAG	CTCTTAATAC	TTTCATGTTT	2040					
2041	CAGAATAATA	GGTTCCGAAA	TAGGCAGGGG	GCATTAAGTG	TTTATACGGG	CACTGTTACT	2100					
2101	CAAGGCACTG	ACCCCGTTAA	AACTTATTAC	CAGTACACTC	CTGTATCATC	AAAAGCCATG	2160					
2161	TATGACGCTT	ACTGGAACGG	TAAATTCAGA	GACTGCGCTT	TCCATTCTGG	CTTTAATGAA	2220					
2221	GATCCATTCTG	TTTGTGAATA	TCAAGGCCAA	TCGTCTGACC	TGCCTCAACC	TCCTGTCAAT	2280					
2281	GCTGGCGGCG	GCTCTGGTGG	TGTTCTGTGT	GGCGGCTCTG	AGGGTGGTGG	CTCTGAGGGT	2340					
2341	GGCGGTTCTG	AGGGTGGCGG	CTCTGAGGGA	GCGGTTCCG	GTGGTGGCTG	TGGTTCGGGT	2400					
2401	GATTTTGATT	ATGAAAAGAT	GGCAAACGCT	AAATAAGGGG	CTATGACCGA	AAATGCCGAT	2460					
2461	GAAAACGCGC	TACAGTCTGA	CGCTAAAGGC	AAACTTGATT	CTGTCGCTAC	TGATTACGGT	2520					
2521	GCTGCTATCG	ATGGTTTCAT	TGGTGACGTT	TCCGGCCTTG	CTAATGGTAA	TGGTGCTACT	2580					
2581	GGTGATTTTG	CTGGCTCTAA	TTCCCAAATG	GCTCAAGTCG	GTGACGGTGA	TAATTCACCT	2640					
2641	TTAATGAATA	ATTTCCGTCA	ATATTTACCT	TCCCTCCCTC	AAATCGGTTGA	ATGTCGCCCT	2700					
2701	TTTGTCTTTA	GCGCTGGTAA	ACCATATGAA	TTTTCTATTG	ATTGTGACAA	ATAAAACTTA	2760					
2761	TTCCGTGGTG	TCTTTGCGTT	TCTTTTATAT	GTTGCCACCT	TTATGTATGT	ATTTTCTACG	2820					
2821	TTTGCTAACA	TACTGCGTAA	TAAGGAGTCT	TAATCATGCC	AGTTCTTTTG	GGTATTCCGT	2880					
2881	TATTATTGCG	TTTCCTCGGT	TTCTTTCTGG	TAACCTTTGT	CGGCTATCTG	CTTACTTTTC	2940					
2941	TTAAAAAGGG	CTTCGGTAAG	ATAGCTATTG	CTATTTTCAT	GTTTCTTTGT	CTTATTATTG	3000					
3001	GGCTTAACTC	AATTCCTTGT	GTTTATCTCT	CTGATATTAG	CGCTCAATTA	CCCTCTGACT	3060					
3061	TTGTTTCAGGG	TGTTCACTTA	ATTCTCCCGT	GTAATGCGCT	TCCCTGTTTT	TATGTTATTG	3120					
3121	TCTCTGTAAA	GGCTGCTATT	TTCATTTTTG	ACGTTAAACA	AAAAATCGTT	TCTTATTTGG	3180					
3181	ATTGGGATAA	ATAATATGGC	TGTTTATTTT	GTAAGTGGCA	AATTAGGCTC	TGGAAAGACG	3240					
3241	CTCGTTAGCG	TTGGTAAGAT	TTAGGATAAA	ATTGTAGCTG	GGTGCAAAAT	AGCAACTAAT	3300					
3301	CTTGATTTAA	GGCTTCAAAA	CCTCCCGCAA	GTCGGGAGGT	TCGCTAAAC	GCCTCGCGTT	3360					
3361	CTTAGAATAC	CGGATAAGCC	TTCTATATCT	GATTTGGGCG	CTATTGGGCG	CGGTAATGAT	3420					
3421	TCCTACGATG	AAAAATAAAA	CGGCTTGCTT	GTTCTCGATG	AGTGCGGTAC	TTGGTTTAAT	3480					
3481	ACCCGTTCTT	GGAATGATAA	GGAAAGACAG	CCGATTATTG	ATTGGTTTCT	ACATGCTCGT	3540					
3541	AAATTAGGAT	GGGATATTAT	CTTCCTTGT	CAGGACTTAT	CTATTGTTGA	TAAACAGGCG	3600					
3601	CGTTCTGCAT	TAGCTGAACA	TGTTGTTTAT	TGTCGTCGTC	TGGACAGAAT	TACTTTACCT	3660					
3661	TTTGTGCGTA	CTTTATATTC	CATTATTACT	GGCTCGAAAA	TGCCTCTGCC	TAAATTACAT	3720					
3721	GTTGGCGTTG	TTAAATATGG	TGATTCTCAA	TTAAGCCCTA	CTGTTGCCG	TTGGCTTTAT	3780					
3781	ACTGGTAAGA	ATTTGTATAA	CGCATATGAT	ACTAAACAGG	CTTTTTCTAG	TAATTATGAT	3840					

FIG. 6-1

SUBSTITUTE SHEET

3841	TCCGGTGTTT	ATTCTTATTT	AACGCCTTAT	TTATCACACG	GTCGGTATTT	CAAAACCATTA	3900
3901	AATTTAGGTC	AGAAGATGAA	ATTAACCTAAA	ATATATTTGA	AAAAGTTTTTC	TCGCGTTTCTT	3960
3961	TGTCTTGCGA	TTGGATTTGC	ATCAGCATTT	ACATATAGTT	ATATAACCCA	ACCTAAGCCG	4020
4021	GAGGTTAAAA	AGGTAGTCTC	TCAGACCTAT	GATTTTGATA	AATTCACCTAT	TGACTCTTCT	4080
4081	CAGCGTCTTA	ATCTAAGCTA	TCGCTATGTT	TTCAAGGATT	CTAAGGGGAAA	ATTAATTAAT	4140
4141	AGCGACGATT	TACAGAAGCA	AGGTTATTCA	CTCACATATA	TTGATTTATG	TACTGTTTCC	4200
4201	ATTAATAAAG	GTAATTCAAA	TGAAATTGTT	AAATGTAATT	AATTTTGTTT	TCTTGATGTT	4260
4261	TGTTTCATCA	TCTTCTTTTG	CTCAGGTAAT	TGAAATGAAT	AATTCGCCTC	TGCGCGATTT	4320
4321	TGTAACCTGG	TATTCAAAGC	AATCAGGCGA	ATCCGTTATT	GTTTCTCCCG	ATGTAAGAGG	4380
4381	TACTGTTACT	GTATATTCAT	CTGACGTTAA	ACCTGAAAAT	CTACGCAATT	TCTTTATTTT	4440
4441	TGTTTTACGT	GCTAATAATT	TTGATATGGT	TGGTTCATT	CCTTCCATAA	TTCAGAAGTA	4500
4501	TAATCCAAAC	AATCAGGATT	ATATTGATGA	ATTGCCATCA	TCTGATAATC	AGGAATATGA	4560
4561	TGATAATTCC	GCTCCTTCTG	GTGGTTTCTT	TGTTCCGCAA	AATGATAATG	TTACTCAAAC	4620
4621	TTTTAAAAAT	AATAACGTTT	GGGCAAGGGA	TTTAATACGA	GTTGTGCAAT	TGTTTGTAAG	4680
4681	GTCTAATACT	TCTAAATCCT	CAAAATGTAT	ATCTATTGAC	GGCTCTAATC	TATTAGTTGT	4740
4741	TAGTGCACCT	AAAGATATTT	TAGATAACCT	TCCTCAATTC	CTTTCTACTG	TTGATTTGCC	4800
4801	AACTGACCAG	ATATTGATTG	AGGGTTTGAT	ATTTGAGGTT	CAGCAAGGTG	ATGCTTTAGA	4860
4861	TTTTTCATTT	GCTGCTGGCT	CTCAGCGTGG	CACTGTTGCA	GGCGGTGTTA	ATACTGACCG	4920
4921	CCTCACCTCT	GTTTTATCTT	CTGCTGGTGG	TTGTTCCGGT	ATTTTTTAATG	GCGATGTTTT	4980
4981	AGGGCTATCA	GTTTCGCGCAT	TAAAGACTAA	TAGCCATTCA	AAAATATTGT	CTGTGCCACG	5040
5041	TATTCTTACG	CTTTCAGGTC	AGAAGGGTTC	TATCTCTGTT	GGCCAGAATG	TCCCTTTTAT	5100
5101	TACTGGTCGT	GTGACTGGTG	AATCTGCCAA	TGTAAATAAT	CCATTTTCTA	CGATTGACGG	5160
5161	TCAAAATGTA	GGTATTTCCA	TGAGCGTTTT	TCCTGTTGCA	ATGGCTGGCG	GTAATATTGT	5220
5221	TCTGGATATT	ACCAGCAAGG	CCGATAGTTT	GAGTTCCTCT	ACTCAGGCAA	GTGATGTTAT	5280
5281	TACTAATCAA	AGAAGTATTG	CTACAACGGT	TAATTTGCGT	GATGGACAGA	CTCTTTTACT	5340
5341	CGGTGGCCTC	ACTGATTATA	ATAAGACTTT	TCAAGATTCT	GGCGTACCGT	TCCTGTCTAA	5400
5401	AATCCCTTTA	ATCGGCCTCC	TGTTTAGCTC	CCGCTCTGAT	TCCAACGAGG	AAAGCACGTT	5460
5461	ATACGTGCTC	GTCAAAGCAA	CCATAGTACG	CGCCCTGTAG	CGGCGCATT	AGCGCGGCGG	5520
5521	GTGTGGTGGT	TACGCGCAGC	GTGACCGCTA	CACTTGCCAG	CGCCCTAGCG	CCCGCTCCTT	5580
5581	TCGCTTTCTT	CCCTTCCTTT	CTCGCCACGT	TCGCCGGCTT	TCCCGTCAA	GCTCTAAATC	5640
5641	GGGGGCTCCC	TTTAGGGTTC	CGATTTAGTG	CTTTACGGCA	CCTCGACCCC	AAAAAACTTG	5700
5701	ATTTGGGTGA	TGGTTACAGT	AGTGGGCCAT	CGCCCTGATA	GACGGTTTTT	CGCCCTTTGA	5760
5761	CGTTGGAGTC	CACGTTCTTT	AATAGTGGAC	TCTTGGAACA	AACTGGAACA	ACACTCAACC	5820
5821	CTATCTCGGG	CTATTCTTTT	GATTTATAAG	GGATTTTGCC	GATTTTCGGAA	CCACCATCAA	5880
5881	ACAGGATTTT	CGCCTGCTGG	GGCAAACCCAG	CGTGGACCGC	TTGCTGCAAC	TCTCTCAGGG	5940
5941	CCAGGCGGTG	AAGGGCAATC	AGCTGTTGCC	CGTCTCGCTG	GTGAAAAGAA	AAACCACCCT	6000
6001	GGCGCCCAAT	ACGCAAACCG	CCTCTCCCCG	CGCGTTGGCC	GATTCATTAA	TGCAGCTGGC	6060
6061	ACGACGAGTT	TCCCGACTGG	AAAGCGGGCA	GTGAGCGCAA	CGCAATTAAT	GTGAGTTAGC	6120
6121	TCACTCATTA	GGCACCCAG	GCTTTACACT	TTATGCTTCC	GGCTCGTATG	TTGTGTGGAA	6180
6181	TTGTGAGCGG	ATAACAATTT	CACACGCCAA	GGAGACAGTC	ATAATGAAAT	ACCTATTGCC	6240
6241	TACGGCAGCC	GCTGGATTGT	TATTACTCGC	TGCCCAACCA	GCCATGGCCG	AGCTCGTGAT	6300
6301	GACCCAGACT	CCAGAATTCC	ATCCGGAATG	AGTGTTAATT	CTAGAACGCG	TAAGCTTGGC	6360
6361	ACTGGCCGTC	GTTTTACAAC	GTCTGAGACTG	GGAAAACCTT	GGCGTTACCC	AACTTAATCG	6420
6421	CCTTGCAGCA	CACCCCCCTT	TCGCCAGCTG	GCCTGAATGG	GAAGAGGCC	GCACCGATCG	6480
6481	CCCTTCCCAA	CAGTTGCGCA	GCCTGAATGG	CGATCTTCTT	TTTGCCTGGT	TTCCGGCACC	6540
6541	AGAAGCGGTG	CCGGAAGAGT	GGCTGGAGTG	CGATCTTCTT	GAGGCCGATA	CGGTCGTCGT	6600
6601	CCCCTCAAAC	TGGCAGATGC	ACGGTTACGA	TGCGCCCATC	TACACCAACG	TAACCTATCC	6660
6661	CATTACGGTC	AATCCGCCGT	TTGTTCCAC	GGAGAATCCG	TCGGGTTGTT	ACTCGCTCAC	6720
6721	ATTTAATGTT	GATGAAAGCT	GGCTACAGGA	AGGCCAGACG	CGAATTAATT	TTGATGGCGT	6780
6781	TCCTATTGGT	TAAAAAATGA	GCTGATTTAA	CAAAAATTTA	ACGCGAATTT	TAACAAAATA	6840
6841	TTAACGTTTA	CAATTTAAAT	ATTTGCTTAT	ACAATCTTCC	TGTTTTTGGG	GCTTTTCTGA	6900
6901	TTATCAACCG	GGGTACATAT	GATTGACATG	CTAGTTTTAC	GATTACCGTT	CATCGATTCT	6960
6961	CTTGTTTGCT	CCAGACTCTC	AGGCAATGAC	CTGATAGCCT	TTGTAGATCT	CTCAAAAATA	7020
7021	GCTACCTTCT	CCGGCATTAA	TTTATCAGCT	AGAACGGTTG	AATATCATAT	TGATGGTGAT	7080
7081	TTGACTGTCT	CCGGCCTTTC	TCACCTTTT	GAATCTTTAC	CTACACATTA	CTCAGGCATT	7140
7141	GCATTTAAAA	TATATGAGGG	TTCTAAAAAT	TTTTATCCTT	GCGTTGAAAT	AAAGGCTTCT	7200
7201	CCCGCAAAAG	TATTACAGGG	TCATAATGTT	TTTGGTACAA	CCGATTTAGC	TTTATGCTCT	7260
7261	GAGGCTTTAT	TGCTTAATTT	TGCTAATTCT	TTGCCTTGCC	TGTATGATTT	ATTGGACGTT	7320

FIG. 6-2

1	AATGCTACTA	CTATTAGTAG	AATTGATGCC	ACCTTTTCAG	CTCGCGCCCC	AAATGAAAAT	60
61	ATAGCTAAAC	AGGTTATTGA	CCATTITGCGA	AATGTATCTA	ATGGTCAAAC	TAAATCTACT	120
121	CGTTTCGAGA	ATTGGGAATC	AACTGTTACA	TGGAATGAAA	CTTCCAGACA	CCGTACTTTA	180
181	GTTGCAATAT	TAAAACATGT	TGAGCTACAG	CACCAGATTG	AGCAATTAAG	CTCTAAGCCA	240
241	TCTGCAAAAA	TGACCTCTTA	TCAAAAAGGAG	CAATTAAGG	TACTCTCTAA	TCCTGACCTG	300
301	TTGGAGTTTG	CTTCCGGTCT	GGTTCGCTTT	GAAGCTCGAA	TTAAAACGCG	ATATTTGAAG	360
361	TCTTTCCGGC	TTCTCTTAA	TCTTTTGTAT	GCAATCCGCT	TTGCTTCTGA	CTATAATAGT	420
421	CAGGGTAAAG	ACCTGATTTT	TGATTTATGG	TCATTCTCGT	TTTCTGAAC	GTTTAAAGCA	480
481	TTTGAGGGGG	ATTCAATGAA	TATTTATGAC	GATTCCGCAG	TATTGGACGC	TATCCAGTCT	540
541	AAACATTTTA	CTATTACCCC	CTCTGGCAAA	ACTTCTTTTG	CAAAAGCCTC	TCGCTATTTT	600
601	GGTTTTTATC	GTCGTCTGGT	AAACGAGGGT	TATGATAGTG	TTGCTCTTAC	TATGCCTCGT	660
661	AATTCTTTT	GGCGTTATGT	ATCTGCATTA	GTTGAATGTG	GTATTCTTAA	ATCTCAACTG	720
721	ATGAATCTTT	CTACCTGTAA	TAATGTTGTT	CCGTTAGTTC	GTTTTATTAA	CGTAGATTTT	780
781	TCTTCCCAAC	GTCCTGACTG	GTATAATGAG	CCAGTCTTAA	AAATCGCATA	AGGTAATTCA	840
841	CAATGATTAA	AGTTGAAATT	AAACCATCTC	AGCAGCTTTG	TACTACTCGT	TCTGGTGTGT	900
901	CTCGTCAGGG	CAAGCCTTAT	TCACTGAATG	ATGAAGGTCA	TTACGTTGAT	TTGGGTAATG	960
961	AATATCCGGT	TCTTGTCAAG	ATTACTCTTG	TTGGTCAGTT	GCCAGCCTAT	GCGCCTGGTC	1020
1021	TGTACACCGT	TCATCTGTCC	TCTTTCAAAG	GAGCAGGTG	CGGTTCCCTT	ATGATTGACC	1080
1081	GTCTGCGGCT	CGTTCCGGCT	AAGTAACATG	GAGCAGGTG	CGGATTTTCA	CACAATTTAT	1140
1141	CAGGCGATGA	TACAAATCTC	CGTTGTACTT	TGTTTTGCGC	TTGGTATAAT	CGCTGGGGGT	1200
1201	CAAAGATGAG	TGTTTTAGTG	TATTTCTTTC	CCTCTTTTCT	TTTAGTTTGG	TGCTTTCGTA	1260
1261	GTGGCATTAC	GTATTTTACC	CGTTTAATGG	AAACTTCCTC	ATGAAAAAGT	CTTTAGTCCT	1320
1321	CAAAGCCTCT	GTAGCCGTTG	CTACCCTCGT	TCCGATGCTG	TCTTTTCGCT	CTGAGGGTGA	1380
1381	CGATCCCGCA	AAAGCGGCCT	TAACTCCCTT	GCAAGCCTCA	GCGACCGAAT	ATATCGGTTA	1440
1441	TGCGTGGGCG	ATGGTTGTTG	TCATTGTCCG	CGCAACTATC	GGTATCAAGC	TGTTTAAAGAA	1500
1501	ATTACCTCG	AAAGCAAGCT	GATAAACCGA	TACAATTAAT	GGCTCCTTTT	GGAGCCTTTT	1560
1561	TTTTTGGAAG	TTTTCAACGT	GAAAAAATTA	TTATTCGCAA	TTCTTTTAGT	TTTCTTTTTC	1620
1621	TATTTCTACT	CCGCTGAAAC	TGTTGAAAGT	TGTTTAGCAA	AACCCCATAC	AGAAAATTCA	1680
1681	TTTACTAACG	TCTGGAAAGA	CGACAAAATC	TTAGATCGTT	ACGCTAACTA	TGAGGGTTGT	1740
1741	CTGTGGAATG	CTACAGGCGT	TGTAGTTTGT	ACTGGTGACG	AAACTCAGTG	TTACGGTACA	1800
1801	TGCGTTTCTA	TTGGGCTTGC	TATCCCTGAA	AATGAGGGTG	GTGGCTCTGA	GGGTGGCGGT	1860
1861	TCTGAGGGTG	GCGGTTCTGA	GGGTGGCGGT	ACTAAACCTC	CTGAGTACGG	TGATACACCT	1920
1921	ATTCCGGGCT	ATACTTATAT	CAACCCTCTC	GACGGCACTT	ATCCGCTTGG	TACTGACCAA	1980
1981	AACCCCGCTA	ATCCTAATCC	TTCTCTTGAG	GAGTCTCAGC	CTCTTAATAC	TTTCATGTTT	2040
2041	CAGAATAATA	GGTTCCGAAA	TAGGCAGGGG	GCATTAACCTG	TTTATACGGG	CACTGTTACT	2100
2101	CAAGGCACTG	ACCCCGTTAA	AACTTATTAC	CAGTACACTC	CTGTATCATC	AAAAGCCATG	2160
2161	TATGACGCTT	ACTGGAACGG	TAAATTCAGA	GACTGCGCTT	TCCATTCTGG	CTTTAATGAA	2220
2221	GATCCATTCTG	TTTGTGAATA	TCAAGGCCAA	TCGTCTGACC	TGCTTCAACC	TGCTGTCAAG	2280
2281	GCTGGCGGCG	GCTCTGGTGG	TGGTCTGGT	GGCGGCTCTG	AGGGTGGTGG	CTCTGAGGGT	2340
2341	GGCGGTTCTG	AGGGTGGCGG	CTCTGAGGGA	GGCGGTTCCG	GTGGTGGCTC	TGGTTCGGGT	2400
2401	GATTTTGATT	ATGAAAAGAT	GGCAAACGCT	AATAAGGGGG	CTATGACCGA	AAATGCCGAT	2460
2461	GAAAACGCGC	TACAGTCTGA	CGCTAAAGGC	AAACTTGATT	CTGTGCTAAC	TGATTACGGT	2520
2521	GCTGCTATCG	ATGGTTTCAT	TGGTGAAGTT	TCCGGCCTTG	CTAATGGTAA	TGGTGTACT	2580
2581	GGTGATTTTG	CTGGCTCTAA	TTCCCAATG	GCTCAAGTCG	GTGACGGTGA	TGATTACACT	2640
2641	TTAATGAATA	ATTTCCGTCA	ATATTTACCT	TCCCTCCCTC	AATCGGTTGA	ATGTCGCCCT	2700
2701	TTTGTCTTTA	GCGCTGGTAA	ACCATATGAA	TTTTCTATTG	ATTGTGACAA	AATAAACTTA	2760
2761	TTCCGTGGTG	TCTTTGCGTT	TCTTTTATAT	GTTGCCACCT	TTATGTATGT	ATTTTCTACG	2820
2821	TTTGCTAACA	TACTGCGTAA	TAAGGAGTCT	TAATCATGCC	AGTTCTTTTG	GGTATTCCGT	2880
2881	TATTATTGCG	TTTCCTCGGT	TTCTTTCTGG	TAACTTTGTG	CGGCTATCTG	CTTACTTTTC	2940
2941	TTAAAAAGGG	CTTCGGTAAG	ATAGCTATTG	CTATTTTCAT	GTTTCTTGCT	CTTATTATTG	3000
3001	GGCTTAACTC	AATTCTTTTG	GGTTATCTCT	CTGATATTAG	CGCTCAATTA	CCCTCTGACT	3060
3061	TTGTTTCAGGG	TGTTCAAGTA	ATTCTCCCGT	CTAATGCGCT	TCCCTGTTTT	TATGTTATTC	3120
3121	TCTCTGTAAA	GGCTGCTATT	TTCAATTTTT	ACGTTAAACA	AAAAATCGTT	TCTTATTTTG	3180
3181	ATTGGGATAA	ATAATATGGC	TGTTTTATTT	GTAACCTGGC	AATTAGGCTC	TGGAAAGACG	3240
3241	CTCGTTAGCG	TTGGTAAGAT	TCAGGATAAA	ATTGTAGCTG	GGTGCAAAAT	AGCAACTAAT	3300
3301	CTTGATTTAA	GGCTTCAAAA	CCTCCCGCAA	GTCGGGAGGT	TCGCTAAAAC	GCCTCGCGTT	3360
3361	CTTAGAATAC	CGGATAAGCC	TTCTATATCT	GATTTGCTTG	CTATTGGGCG	CGGTAATGAT	3420
3421	TCCTACGATG	AAAATAAAAA	CGGCTTGCTT	GTTCTCGATG	AGTGCGGTAC	TTGGTTTAAAT	3480
3481	ACCCGTTCTT	GGAATGATAA	GGAAAGACAG	CCGATTATTG	ATTGGTTTCT	ACATGCTCGT	3540
3541	AAATTAAGGAT	GGAATATTAT	TTTTCTTGTT	CAGGACTTAT	CTATTGTTGA	TAAACAGGCG	3600
3601	CGTTCTGCAT	TAGCTGAACA	TGTTGTTTAT	TGTCGTCGTC	TGGACAGAAT	TACTTTACCT	3660
3661	TTTGTGCGTA	CTTTATATTC	TCTTATTACT	GGCTCGAAAA	TGCCTCTGCC	TAAATTTACAT	3720
3721	GTTGGCGTTG	TTAAATATGG	CGATTCTCAA	TTAAGCCCTA	CTGTTGAGCG	TTGGCTTTAT	3780

FIG. 7-1

3781	ACTGGTAAGA	ATTTGTATAA	CGCATATGAT	ACTAAACAGG	CTTTTTCTAG	TAATTATGAT	3840
3841	TCCGGTGT	ATTCTTATTT	AACGCCCTTAT	TTATCACACG	GTCGGTATTT	CAAACCATTA	3900
3901	AATTTAGGTC	AGAAGATGAA	GCTTACTAAA	ATATATTTGA	AAAAGTTTTT	ACGCGTTCTT	3960
3961	TGTCTTGCGA	TTGGATTTGC	ATCAGCATTT	ACATATAGTT	ATATAACCCA	ACCTAAGCCG	4020
4021	GAGGTTAAAA	AGGTAGTCTC	TCAGACCTAT	GATTTTGATA	AATTCACAT	TGACTCTTCT	4080
4081	CAGCGTCTTA	ATCTAAGCTA	TCGCTATGTT	TTCAAGGATT	CTAAGGGAAA	ATTAATTAAT	4140
4141	AGCGACGATT	TACAGAAGCA	AGGTTATTCA	CTCACATATA	TTGATTTATG	TACTGTTTCC	4200
4201	ATTAATAAAG	GTAATTCAAA	TGAAATTGTT	AAATGTAATT	AATTTTGTTT	TCTTGATGTT	4260
4261	TGTTTCATCA	TCTTCTTTTG	CTCAGGTAAT	TGAAATGAAT	AATTCGCCCT	TGCGCGATTT	4320
4321	TGTAACCTTG	TATTCAAAGC	AATCAGGCGA	ATCCGTTATT	GTTTCTCCCG	ATGTAAAAGG	4380
4381	TACTGTTACT	GTATATTTCAT	CTGACGTTAA	ACCTGAAAAT	CTACGCAATT	TCTTTATTTT	4440
4441	TGTTTTACGT	GCTAATAATT	TTGATATGGT	TGGTTCAATT	CCTTCCATAA	TTCAGAAGTA	4500
4501	TAATCCAAAC	AATCAGGATT	ATATTGATGA	ATTGCCATCA	TCTGATAATC	AGGAATATGA	4560
4561	TGATAATCC	GCTCCTTCTG	TGGTTTTCTT	TGTTCCGCAA	AATGATAATG	TTACTCAAAC	4620
4621	TTTTAAATTT	AATAACGTTT	GCGCAAAGGA	TTTAATACGA	GTTGTGCAAT	TGTTTGTAAA	4680
4681	GTCTAATACT	TCTAAATCCT	CAAATGTATT	ATCTATTGAC	GGCTCTAATC	TATTAGTTGT	4740
4741	TAGTGCACCT	AAAGATATTT	TAGATAACCT	TCCTCAATTC	CTTTCTACTG	TTGATTTGCC	4800
4801	AACGTGACCA	ATATTGATTG	AGGGTTTGAT	ATTTGAGGTT	CAGCAAGGTG	ATGCTTTAGA	4860
4861	TTTTTCAATT	GCTGCTGGCT	CTCAGCGTGG	CACGTGTTGA	GGCGGTGTTA	ATACTGACCG	4920
4921	CCTCACCTCT	GTTTTATCTT	CTGCTGGTGG	TTCGTTCCGT	ATTTTTAATG	GCGATGTTTT	4980
4981	AGGGCTATCA	GTTTCGCGCAT	TAAAGACTAA	TAGCCATTCA	AAAAATATTG	CTGTGCCACG	5040
5041	TATTTCTTACG	CTTTCAGGTC	AGAAGGGTTC	TATCTCTGTT	GGCCAGAATG	TCCCTTTTAT	5100
5101	TACTGGTCGT	GTGACTGGTG	AATCTGCCAA	TGTAAATAAT	CCATTTTCTA	CGATTGAGCG	5160
5161	TCAAAATGTA	GGTATTTCCA	TGAGCGTTTT	TCCTGTTGCA	ATGGCTGGCG	GTAATATTGT	5220
5221	TCTGGATATT	ACCAGCAAGG	CCGATAGTTT	GAGTTCTTCT	ACTCAGGCAA	GTGATGTTAT	5280
5281	TACTAATCAA	AGAAGTATTG	CTACAACGTT	TAATTTGCGT	GATGGACAGA	CTCTTTTACT	5340
5341	CGGTGGCCTC	ACTGATTATA	AAAACACTTC	TCAAGATTCT	GGCGTACCGT	TCTGTCTTAA	5400
5401	AATCCCTTTA	ATCGGCCTCC	TGTTTAGCTC	CCGCTCTGAT	TCCAACGAGG	AAAGCAGGTT	5460
5461	ATACGTGCTC	GTCAAAGCAA	CCATAGTACG	CGCCCTGTAG	CGGCGCATT	AGCGCGGCGG	5520
5521	GTGTGGTGGT	TACGCGCAGC	GTGACCGCTA	CACTTGGCAG	CGCCCTAGCG	CCCGCTCCTT	5580
5581	TCGCTTTCTT	CCCTTCTCTT	CTCGCCACGT	TCGCGGCTT	TCCCGTCAAA	GCTCTAAATC	5640
5641	GGGGGCTCCC	TTTAGGGTTT	CGATTATAGT	CTTTACGGCA	CCTCGACCCC	AAAAAACTTG	5700
5701	ATTTGGGTGA	TGGTTACAGT	AGTGGGCCAT	CGCCCTGATA	GACGGTTTTT	CGCCCTTTGA	5760
5761	CGTTGGAGTC	CACGTTCTTT	AATAGTGGAC	TCTTGTTCCT	AACTGGAACA	ACACTCAACC	5820
5821	CTATCTCGGG	CTATTCTTTT	GATTTATAAG	GGATTTTGCC	GATTTGCGAA	CCACCATCAA	5880
5881	ACAGGATTTT	CGCCTGCTGG	GGCAAACCA	CGTGGACCGC	TTGCTGCAAC	TCTCTCAGGG	5940
5941	CCAGGCGGTG	AAGGGCAATC	AGCTGTTGCC	CGTCTCGCTG	GTGAAAAGAA	AAACCACCCT	6000
6001	GGCGCCCAAT	ACGCAAAACG	CCTCTCCCGG	CGCGTTGGCC	GATTCATTAA	TGCAGCTGGC	6060
6061	ACGACAGGTT	TCCCGACTGG	AAAGCGGGCA	GTGAGCGCAA	CGCAATTAAT	CGGAGTTAGC	6120
6121	TCACTCATT	GGCACCCAG	GCTTTACACT	TTATGCTTCC	GGCTCGTATG	TTGTGTGGAA	6180
6181	TTGTGAGCGG	ATAACAATTT	CACACGCGTC	ACTTGGCACT	GGCCGTCTGT	TTACAACGTC	6240
6241	GTGACTGGGA	AAACCCTGGC	GTTACCCCA	CTTTGTACAT	GGAGAAAATA	AAGTGAAACA	6300
6301	AAGCACTATT	GCACTGGCAC	TCTTACCGTT	ACCGTTACTG	TTTACCCCTG	TGACAAAAGC	6360
6361	CGCCAGGTC	CAGCTGCTCG	AGTCAAGCCT	ATTGTGCCCA	GGGGATTGTA	CTAGTGGATC	6420
6421	CTAGGCTGAA	GGCGATGACC	CTGCTAAGGC	TGCATTCAAT	AGTTTACAGG	CAAGTGCTAC	6480
6481	TGAGTACATT	GGCTACGCTT	GGGCTATGGT	AGTAGTTATA	GTTGGTGCTA	CCATAGGGAT	6540
6541	TAAATTATTC	AAAAAGTTTA	CGAGCAAGGC	TTCTTAAGCA	ATAGCGAAGA	GGCCCGCACC	6600
6601	GATCGCCCTT	CCCAACAGTT	GCGCAGCCTG	AATGGCGAAT	GGCGCTTTGC	CTGGTTTCCG	6660
6661	GCACCGAAG	CGGTGCCGGA	AAGCTGGCTG	GAGTGCATC	TTCTTGAGGC	CGATACGGTC	6720
6721	GTCGTCCCTT	CAAACCTGGC	GATGCACGGT	TACGATGCGC	CCATCTACAC	CAACGTAACC	6780
6781	TATCCCATTA	CGGTCAATCC	GCCGTTTGTT	CCCACGGAGA	ATCCGACGGG	TTGTTACTCG	6840
6841	CTCACATTTA	ATGTTGATGA	AAGCTGGCTA	CAGGAAGGCC	AGACGCGAAT	TATTTTTGAT	6900
6901	GGCGTTCTTA	TTGGTTAAAA	AATGAGCTGA	TTTAACAAAA	ATTTAACGCG	AATTTTAAAC	6960
6961	AAATATTAAC	GTTTACAATT	TAAATATTTG	CTTATACAAT	CTTCCTGTTT	TTGGGGCTTT	7020
7021	TCTGATTATC	AACCGGGGTA	CATATGATTG	ACATGCTAGT	TTTACGATTA	CCGTTTCATC	7080
7081	ATTCTCTTGT	TTGCTCCAGA	CTCTCAGGCA	ATGACCTGAT	AGCCTTTGTA	GATCTCTCAA	7140
7141	AAATAGCTAC	CCTCTCCGGC	ATTAATTTAT	CAGCTAGAAC	GGTTGAATAT	CATATTGATG	7200
7201	GTGATTTGAC	TGTCTCCGGC	CTTTCTCACC	CTTTTGAATC	TTTACCTACA	CATTACTCAG	7260
7261	GCATTGCATT	TAAAATATAT	GAGGGTTCTA	AAAATTTTTT	TCCTTGCGTT	GAAATAAAGG	7320
7321	CTTCTCCCGC	AAAAGTATTA	CAGGGTCATA	ATGTTTTTGG	TACAACCGAT	TTAGCTTTAT	7380
7381	GCTCTGAGGC	TTTATTGCTT	AATTTTGCTA	ATTCTTTGCC	TTGCCTGTAT	GATTTATTGG	7440
7441	ACGTT						7445

FIG. 7-2

	10	20	30	40	50	60
1	AATGCTACTA	CTATTAGTAG	AATTGATGCC	ACCTTTTCAG	CTCGCGCCCC	AAATGAAAAT
61	ATAGCTAAAC	AGGTTATTGA	CCATTTGCGA	AATGTATCTA	ATGGTCAAAC	TAAATCTACT
121	CGTTTCGAGA	ATTGGGAATC	AACTGTTACA	TGGAATGAAA	CTTCCAGACA	CCGTACTTTA
181	GTTGCAATAT	TAAAACATGT	TGAGCTACAG	CACCAGATTG	AGCAATTAAG	CTCTAAGCCA
241	TCTGCAAAAA	TGACCTCTTA	TCAAAAGGAG	CAATTAAGG	TACTCTCTAA	TCCTGACCTG
301	TTGGAAGTTG	CTTCCGGTCT	GGTTTCGTTT	GGAAGCTCGAA	TTAAAACGCG	ATATTTGAAG
361	TCTTTCCGGC	TTCTCTTAA	TCTTTTTGAT	GCAATCCGCT	TTGCTTCTGA	CTATAATAGT
421	CAGGGTAAAG	ACCTGATTTT	TGATTTATGG	TCATTCTCGT	TTTCTGAACT	GTTTAAAGCA
481	TTTGAGGGGG	ATTCAATGAA	TATTTATGAC	GATTCCGCAG	TATTGGACGC	TATCCAGTCT
541	AAACATTTTA	CTATTACCCC	CTCTGGCAAA	ACTTCTTTTG	CAAAAGCCTC	TCGCTATTTT
601	GGTTTTTATC	GTCGTCTGGT	AAACGAGGGT	TATGATAGTG	TTGCTCTTAC	TATGCCTCGT
661	AATTCCTTTT	GGCGTTATGT	ATCTGCATTA	GTTGAATGTG	GTATTCCTAA	ATCTCAACTG
721	ATGAATCTTT	CTACCTGTAA	TAATGTTGTT	CCGTTAGTTT	GTTTTATTAA	CGTAGATTTT
781	TCTTCCCAAC	GTCCTGACTG	GTATAATGAG	CCAGTTCTTA	AAATCGCATA	AGGTAATTCA
841	CAATGATTAA	AGTTGAAATT	AAACCATCTC	AAGCCCAATT	TACTACTCGT	TCTGGTGTGT
901	CTCGTCAGGG	CAAGCCTTAT	TCACTGAATG	AGCAGCTTTG	TTACGTTGAT	TTGGGTAATG
961	AATATCCGGT	TCTTGTCAAG	ATTACTCTTG	ATGAAGGTCA	GCCAGCCTAT	GCGCCTGGTC
1021	TGTACACCGT	TCATCTGTCC	TCTTTCAAAG	TTGGTCAGTT	CGGTTCCCTT	ATGATTGACC
1081	GTCTGCGCCT	CGTTCCGGCT	AAGTAACATG	GAGCAGGTCG	CGGATTTTGA	CACAATTTAT
1141	CAGGCGATGA	TACAAATCTC	CGTTGTACTT	TGTTTCGCGC	TTGGTATAAT	CGCTGGGGGT
1201	CAAAGATGAG	TGTTTTAGTG	TATTTCTTCG	CCTCTTTCTG	TTTAGGTTGG	TGCCTTCGTA
1261	GTGGCATTAC	GTATTTTACC	CGTTTAATGG	AAACTTCCTC	ATGAAAAAGT	CTTTAGTCTT
1321	CAAAAGCCTC	GTAGCCGTTG	CTACCCTCGT	TCCGATGCTG	TCTTTCGCTG	CTGAGGGTGA
1381	CGATCCCGCA	AAAGCGGCCT	TTAACTCCCT	GCAAGCCTCA	GCGACCGAAT	ATATCGGTTA
1441	TGCGTGGGCG	ATGGTTGTTG	TATTTGTCGG	CGCAACTATC	GGTATCAAGC	TGTTTAAGAA
1501	ATTCACCTCG	AAAGCAAGCT	GATAAACCGA	TACAATTAAT	GGCTCCTTTT	GGAGCCTTTT
1561	TTTTTGAGAG	TTTTCAACGT	GAAAAAATTA	TTATTCGCAA	TTCTTTTAGT	TGTTCTTTTC
1621	TATTTCTACT	CCGCTGAAAC	TGTTGAAAGT	TGTTTAGCAA	AACCCCATAC	AGAAAATTCA
1681	TTTACTAACG	TCTGGAAAGA	CGACAAAATC	TTAGATCGTT	ACGCTAATA	TGAGGGTTGT
1741	CTGGTGAATG	CTACAGGCGT	TGTAGTTTGT	ACTGGTGACG	AAACTCAGTG	TTACGGTACA
1801	TGGGTTCTTA	TTGGGCTTGC	TATCCCTGAA	AATGAGGGTG	GTGGCTCTGA	GGGTGGCGGT
1861	TCTGAGGGTG	GCGGTTCTGA	GGGTGGCGGT	ACTAAACCTC	CTGAGTACGG	TGATACACCT
1921	ATTCGGGGCT	ATACTTATAT	CAACCCTCTC	GACGGCACTT	ATCCGCCTGG	TACTGAGCAA
1981	AACCCCGCTA	ATCCTAATCC	TTCTCTTGAG	GAGTCTCAGC	CTCTTAATAC	TTTCATGTTT
2041	CAGAATAATA	GGTTCGAAAT	TAGGCAGGGG	GCATTAACCT	TTTATACGGG	CACTGTTACT
2101	CAAGGCACCT	ACCCCGTTAA	AACTTATTAC	CAGTACATCT	CTGTATCATC	AAAAGCCATG
2161	TATGACGCTT	ACTGGAACGG	TAAATTGAGA	GACTGCGCTT	TCCATTCTGG	CTTTAATGAA
2221	GATCCATTCT	TTTGTGAATA	TCAAGGCCAA	TCGTCTGACC	TGCCTCAACC	TCCTGTCAAT
2281	GCTGGCGGCG	CGTCTGGTGG	TGGTCTGGT	GGCGGCTCTG	AGGGTGGTGG	CTCTGAGGGT
2341	GGCGGTTCTG	AGGGTGGCGG	CTCTGAGGGA	GGCGGTTCCG	GTGGTGGCTC	TGGTTCGGGT
2401	GATTTTGATT	ATGAAAAGAT	GGCAAACGCT	AATAAGGGGG	CTATGACCGA	AAATGCCGAT
2461	GAAAACGCGC	TACAGTCTGA	CGCTAAAGGC	AAACTTGATT	CTGTGCTGAC	TGATTACGGT
2521	CTGTCTATCG	ATGGTTTCAT	TGGTGACGTT	TCCGGCCTTG	CTAATGGTAA	TGGTGCTACT
2581	GGTGATTTTG	CTGGCTCTAA	TTCCCAAATG	GCTCAAGTCG	GTGACGGTGA	TAATTCACCT
2641	TTAATGAATA	ATTTCCGTCA	ATATTTACCT	TCCCTCCCTC	AATCGGTTGA	ATGTCGCCCT
2701	TTTGTCTTTA	GCGCTGGTAA	ACCATATGAA	TTTTCTATTG	ATTGTGACAA	AATAAACTTA
2761	TTCCGTGGTG	TCTTTGCGTT	TCTTTTATAT	GTTGCCACCT	TTATGTATGT	ATTTTCTACG
2821	TTTGCTAACA	TACTGCGTAA	TAAGGAGTCT	TAATCATGCC	AGTTCTTTTG	GGTATTCCGT
2881	TATTATTGCG	TTTCTCTGGT	TTCTTCTGTT	TAACCTTGTG	CGGCTATCTG	CTTACTTTTC
2941	TTAAAAAGGG	CTTCGGTAAG	ATAGCTATTG	CTATTTTCATT	GTTTCTTGCT	CTTATTATTG
3001	GGCTTAACCT	AATTCCTGTG	GGTTATCTCT	CTGATATTAG	CGCTCAATTA	CCCTCTGACT
3061	TTGTTTCAGG	TGTTCAAGTT	ATTCTCCCGT	CTAATGCGCT	TCCCTGTTTT	TATGTTATTG
3121	TCTCTGTAAA	GGCTGCTATT	TTTCAATTTG	ACGTTAAACA	AAAAATCGTT	TCTTATTTGG
3181	ATTGGGATAA	ATAATATGGC	TGTTTATTTT	GTAACCTGGC	AATTAGGCTC	TGGAAAGACG
3241	CTCGTTAGCG	TTGGTAAGAT	TTAGGATAAA	ATTGTAGCTG	GGTGCAAAAT	AGCAACTAAT
3301	CTTGATTTAA	GGCTTCAAAA	CCTCCCGCAA	GTCGGGAGGT	TCGCTAAAAC	GCCTCGCGTT
3361	CTTAGAATAC	CGGATAAGCC	TTCTATATCT	GATTTTGCTG	CTATTGGGCG	CGGTAATGAT
3421	TCCTACGATG	AAAATAAAAA	CGGCTTGCTT	GTTCTCGATG	AGTGCGGTAC	TCGTTTAAAT
3481	ACCCGTTCTT	GGAATGATAA	GGAAAGACAG	CCGATTATTG	ATTGGTTTCT	ATGATCTCGT
3541	AAATTAGGAT	GGGATATTAT	TTTTCTTGTT	CAGGACTTAT	CTATTGTTGA	TAAACAGGCG
3601	CGTTCTGCAT	TAGCTGAACA	TGTTGTTTTAT	TGTCGTCGTC	TGGACAGAAT	TACTTTACCT
3661	TTTGTCGGTA	CTTTATATTC	TCTTATTACT	GGCTCGAAAA	TGCCTCTGCC	TAAATTACAT
3721	GTTGGCGTTG	TTAAATATGG	CGATTCTCAA	TTAAGCCCTA	CTGTTGAGCG	TTGGCTTTAT
3781	ACTGGTAAGA	ATTTGTATAA	CGCATATGAT	ACTAAACAGG	CTTTTTCTAG	TAATTATGAT

FIG. 8-1

SUBSTITUTE SHEET

3841	TCCGGTGTTT	ATTCTTATTT	AACGCCTTAT	TTATCACACG	GTCGGTATTT	CAAACCATTA	3900
3901	AATTTAGGTC	AGAAGATGAA	GCTTACTAAA	ATATATTTGA	AAAAGTTTTT	ACGCGTTCTT	3960
3961	TGTCTTGCGA	TTGGATTTGC	ATCAGCATTT	ACATATAGTT	ATATAACCCA	ACCTAAGCCG	4020
4021	GAGGTTAAAA	AGGTAGTCTC	TCAGACCTAT	GATTTTGATA	AATTCACAT	TGACTCTTCT	4080
4081	CAGCGTCTTA	ATCTAAGCTA	TCGCTATGTT	TTCAAGGATT	CTAAGGGAAA	ATTAATTAAT	4140
4141	AGCGACGATT	TACAGAAGCA	AGGTTATTCA	CTCACATATA	TTGATTTATG	TACTGTTTCC	4200
4201	ATTAATAAAG	GTAATTCAAA	TGAAATTGTT	AAATGTAATT	AATTTTGTTT	TCTTGATGTT	4260
4261	TGTTTCATCA	TCTTCTTTTG	CTCAGGTAAT	TGAAATGAAT	AATTCGCCTC	TGCGCGATTT	4320
4321	TGTAAC TTGG	TATTCAAAGC	AATCAGGCGA	ATCCGTTATT	GTTTCTCCCG	ATGTAAAAGG	4380
4381	TACTGTTACT	GTATATTCAT	CTGACGTTAA	ACCTGAAAAT	CTACGCAATT	TCTTTATTTT	4440
4441	TGTTTTACGT	GCTAATAATT	TTGATATGGT	TGGTTCAATT	CCTTCCATAA	TTCAGAAGTA	4500
4501	TAATCCAAAC	AATCAGGATT	ATATTGATGA	ATTGCCATCA	TCTGATAATC	AGGAATATGA	4560
4561	TGATAATTCC	GCTCCTTCTG	GTGGTTTCTT	TGTTCCGCAA	AATGATAATG	TTACTCAAAC	4620
4621	TTTTAAAAAT	AATAACGTTT	GGGCAAAAGG	TTTAATACGA	GTTGTGCAAT	TGTTTGTAAG	4680
4681	GTCTAATACT	TCTAAATCCT	CAAATGTATT	ATCTATTGAC	GGCTCTAATC	TATTAGTTGT	4740
4741	TAGTGCACCT	AAAGATATTT	TAGATAACCT	TCCTCAATT	CTTTCTACTG	TTGATTTGCC	4800
4801	AACTGACCAG	ATATTGATTG	AGGGTTTGAT	ATTTGAGGTT	CAGCAAGGTG	ATGCTTTAGA	4860
4861	TTTTTCATTT	GCTGCTGGCT	CTCAGCGTGG	CACTGTTGCA	GGCGGTGTTA	ATACTGACCG	4920
4921	CCTCACCTCT	GTTTTATCTT	CTGCTGGTGG	TTGTTTCGGT	ATTTTTAATG	GCGATGTTTT	4980
4981	AGGGCTATCA	GTTGCGCAT	TAAAGACTAA	TAGCCATTCA	AAAATATTGT	CTGTGCCACG	5040
5041	TATTCCTACG	CTTTCAGGTC	AGAAGGGTTC	TATCTCTGTT	GGCCAGAATG	TCCCTTTTAT	5100
5101	TACTGGTCGT	GTGACTGGTG	AATCTGCCAA	TGTAAATAAT	CCATTTTACA	CGATTGAGCG	5160
5161	TCAAAATGTA	GGTATTTCCA	TGAGCGTTTT	TCCTGTTGCA	ATGGCTGGCG	GTAATATTGT	5220
5221	TCTGGATATT	ACCAGCAAGG	CCGATAGTTT	GAGTTCCTCT	ACTCAGGCAA	GTGATGTTAT	5280
5281	TACTAATCAA	AGAAGTATTG	CTACAACGGT	TAATTTGCGT	GATGGACAGA	CTCTTTTACT	5340
5341	CGGTGGCCTC	ACTGATTATA	AAAACACTTC	TCAAGATTCT	GGCGTACCGT	TCCTGTCTAA	5400
5401	AATCCCTTTA	ATCGGCCTCC	TGTTTAGCTC	CCGCTCTGAT	TCCAACGAGG	AAAGCACGTT	5460
5461	ATACGTGCTC	GTCAAAGCAA	CCATAGTACG	CGCCCTGTAG	CGGCGCATT	AGCGCGGCGG	5520
5521	GTGTGGTGGT	TACGCGCAGC	GTGACCGCTA	CACTTGCCAG	CGCCCTAGCG	CCCCTCTCTT	5580
5581	TCGCTTTCTT	CCCTTCTCTT	CTCGCCACGT	TCGCGGCTT	TCCCCGTCAA	GCTCTAAATC	5640
5641	GGGGGCTCCC	TTTAGGGTTC	CGATTTATGT	CTTTACGGCA	CCTCGACCCC	AAAAAACTTG	5700
5701	ATTTGGGTGA	TGGTTACAGT	AGTGGGCCAT	CGCCCTGATA	GACGGTTTTT	CGCCCTTTGA	5760
5761	CGTTGGAGTC	CACGTTCTTT	AATAGTGGAC	TCTTGTTCCA	AACTGGAACA	ACACTCAACC	5820
5821	CTATCTCGGG	CTATTCTTTT	GATTTATAAG	GGATTTTGCC	GATTTGCGAA	CCACCATCAA	5880
5881	ACAGGATTTT	CGCCTGCTGG	GGCAAACCGA	CGTGGACCGC	TTGCTGCAAC	TCTCTCAGGG	5940
5941	CCAGGCGGTG	AAGGGCAATC	AGCTGTTGCC	CGTCTCGCTG	GTGAAAAGAA	AAACCACCCT	6000
6001	GGCGCCCAAT	ACGCAAAACG	CCTCTCCCGG	CGCGTTGGCC	GATTCATTAA	TGCAGTGGC	6060
6061	ACGACAGGTT	TCCCGACTGG	AAAGCGGGCA	GTGAGCGCAA	CGCAATTAAT	GTGAGTTAGC	6120
6121	TCACTCATT	GGCACCCAG	GCTTTACACT	TTATGCTTCC	GGCTCGTATG	TTGTGTGGAA	6180
6181	TTGTGAGCGG	ATAACAATTT	CACACGCGTC	ACTTGGCACT	GGCCGTCGTT	TTACAACGTC	6240
6241	GTGACTGGGA	AAACCCTGGC	GTTACCCAAG	CTTTGTACAT	GGAGAAAATA	AAGTGAAACA	6300
6301	AAGCACTATT	GCACTGGCAC	TCTTACCGTT	ACTGTTTACC	CCTGTGGCAA	AAGCCTATGG	6360
6361	GGGGTTTATG	CTTCTGAGGC	ATCCGGGAGC	TGAAGGCGAT	GACCTTGCTA	AGGCTGCATT	6420
6421	CAATAGTTTA	CAGGCAAGTG	CTACTGAGTA	CATTGGCTAC	GCTTGGGCTA	TGGTAGTAGT	6480
6481	TATAGTTGGT	GCTACCATAG	GGATTAAATT	ATTCAAAAAG	TTTACGAGCA	AGGCTTCTTA	6540
6541	AGCAATAGCG	AAGAGGCCCG	CACCGATCGC	CCTTCCCAAC	AGTTGCGCAG	CCTGAATGGC	6600
6601	GAATGGCGCT	TTGCCTGGTT	TCCGGCACCA	GAAGCGGTGC	CGGAAAGCTG	GCTGGAGTGC	6660
6661	GATCTTCTCT	AGGCCGATAC	GGTCGTCGTC	CCCTCAAAC	GGCAGATGCA	CGGTTACGAT	6720
6721	CGCGCCATCT	ACACCAACGT	AACCTATCCC	ATTACGGTCA	ATCCGCCGTT	TGTTCCACAG	6780
6781	GAGAATCCGA	CGGGTTGTTA	CTCGCTCACA	TTTAATGTTG	ATGAAAGCTG	GCTACAGGAA	6840
6841	GGCCAGACGC	GAATTATTTT	TGATGGCGTT	CCTATTGGTT	AAAAAATGAG	CTGATTTAAC	6900
6901	AAAAATTTAA	CGCGAATTTT	AACAAAATAT	TAACGTTTAC	AATTTAAATA	TTTGCTTATA	6960
6961	CAATCTTCTT	GTTTTTGGGG	CTTTTCTGAT	TATCAACCGG	GGTACATATG	ATTGACATGC	7020
7021	TAGTTTTACG	ATTACCGTTC	ATCGATTCTC	TTGTTTGCTC	CAGACTCTCA	GGCAATGACC	7080
7081	TGATAGCCTT	TGTAGATCTC	TCAAAAATAG	CTACCTCTCT	CGGCATTAA	TTATCAGCTA	7140
7141	GAACGGTTGA	ATATCATATT	GATGGTGATT	TGACTGTCTC	CGGCCTTTCT	CACCCCTTTG	7200
7201	AATCTTTACC	TACACATTAC	TCAGGCATTG	CATTTAAAAT	ATATGAGGGT	TCTAAAAAAT	7260
7261	TTTATCCTTG	CGTTGAAATA	AAGGCTTCTC	CCGCAAAAGT	ATTACAGGGT	CATAATGTTT	7320
7321	TTGGTACAAC	CGATTTAGCT	TTATGCTCTG	AGGCTTTATT	GCTTAATTTT	GCTAATTCTT	7380
7381	TGCCTTGCCT	GTATGATTTA	TTGGACGTT				7409

FIG. 8-2

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	10	20	30	40	50	60	
1	AATGCTACTA	CTATTAGTAG	AATTGATGCC	ACCTTTTTCAG	CTCGCGCCCC	AAATGAAAAT	60
61	ATAGCTAAAC	AGGTTATTGA	CCATTTGCGA	AATGTATCTA	ATGGTCAAAAC	TAAATCTACT	120
121	CGTTCCGAGA	ATTGGGAATC	AACTGTTACA	TGGAATGAAA	CTTCCAGACA	CCGTACTTTA	180
181	GTTGCATATT	TAAAACATGT	TGAGCTACAG	CACCAGATTC	AGCAATTAAG	CTCTAAGCCA	240
241	TCTGCAAAAA	TGACCTCTTA	TCAAAAGGAG	CAATTAAGG	TACTCTCTAA	TCCTGACCTG	300
301	TTGGAAGTTTG	CTTCCGGTCT	GGTTTCGCTTT	GAAGCTCGAA	TTAAACCGCG	ATATTTGAAG	360
361	TCTTTTCGGGC	TTCCTCTTAA	TCTTTTTGAT	GCAATCCGCT	TTGCTTCTGA	CTATAATAGT	420
421	CAGGGTAAAG	ACCTGATTTT	TGATTTATGG	TCATTCTCGT	TTTCTGAACT	GTTTAAAGCA	480
481	TTTGAGGGGG	ATTCAATGAA	TATTTATGAC	GATTCGCGAG	TATTGGACGC	TATCCAGTCT	540
541	AAACATTTTA	CTATTACCCC	CTCTGGCAAA	ACTTCTTTTG	CAAAAGCCTC	TCGCTATTTT	600
601	GGTTTTTATC	GTCGTCTGGT	AAACGAGGGT	TATGATAGTG	TTGCTCTTAC	TATGCCTCGT	660
661	AATTCCTTTT	GGCGTTATGT	ATCTGCATTA	GTTGAATGTG	GTATTCCTAA	ATCTCAACTG	720
721	ATGAATCTTT	CTACCTGTAA	TAATGTTGTT	CCGTTAGTTC	GTTTTATTAA	CGTAGATTTT	780
781	TCTTCCCAAC	GTCCTGACTG	GTATAATGAG	CCAGTTCCTA	AAATCGCATA	AGGTAATTCT	840
841	CAATGATTAA	AGTTGAAATT	AAACCATCTC	AAGCCCAATT	TACTACTCGT	TCTGGTGTTC	900
901	CTCGTCAGGG	CAAGCCTTAT	TCACTGAATG	AGCAGCTTTG	TTACGTTGAT	TTGGGTAATG	960
961	AATATCCGGT	TCTTGTCAAG	ATTACTCTTG	ATGAAGGTCA	GCCAGCCTAT	GCGCCTGGTC	1020
1021	TGTACACCGT	TCATCTGTCC	TCTTTCAAAG	TTGGTCAGTT	CGGTTCCCTT	ATGATTGACC	1080
1081	GTCTGCGCCT	CGTTCCGGCT	AAGTAACATG	GAGCAGGTCG	CGGATTTTCA	CACATTTTAT	1140
1141	CAGGCGATGA	TACAAATCTC	CGTTGTACTT	TGTTTCGCGC	TTGGTATAAT	CGCTGGGGGT	1200
1201	CAAAGATGAG	TGTTTTAGTG	TATTTCTTCG	CCTCTTTCGT	TTTAGGTTGG	TGCCTTCGTA	1260
1261	GTGGCATTAC	GATTTTTACC	CGTTTAATGG	AAACTTCCTC	ATGAAAAAGT	CTTTAGTCCT	1320
1321	CAAAGCCTCT	GTAGCCGTTG	CTACCCTCGT	TCCGATGCTG	TCTTTCGCTG	CTGAGGGTGA	1380
1381	CGATCCCGCA	AAAGCGGCCCT	TTAACTCCCT	GCAAGCCTCA	GCGACCGAAT	ATATCGGTTA	1440
1441	TGCGTGGGCG	ATGGTTGTTG	TCATTGTCGG	CGCAACTATC	GGTATCAAGC	TGTTTAAAGAA	1500
1501	ATTCACCTCG	AAAGCAAGCT	GATAAACCGA	TACAATTAAA	GGCTCCTTTT	GGAGCCTTTT	1560
1561	TTTTTGAGAG	TTTTCAACGT	GAAAAAATTA	TATTTTCGAA	TTCTTTTAGT	TGTTCTTTTC	1620
1621	TATTTCTACT	CCGCTGAAAC	TGTTGAAAGT	TGTTTAGCAA	AACCCCATAC	AGAAAAATTCA	1680
1681	TTTACTAACG	TCTGGAAAGA	CGACAAAAC	TTAGATCGTT	ACGCTAACTA	TGAGGGTGTG	1740
1741	CTGTGGAATG	CTACAGGCGT	TGTAGTTTGT	ACTGGTGACG	AAACTCAGTG	TTACGGTACA	1800
1801	TGGGTTCTTA	TTGGGCTTGC	TATCCCTGAA	AATGAGGGTG	GTGGCTCTGA	GGGTGGCGGT	1860
1861	TCTGAGGGTG	GCGGTTCTGA	GGGTGGCGGT	ACTAAGACCTC	CTGAGTACGG	TGATACACCT	1920
1921	ATTCCTGGGT	ATACCTTATAT	CAACCTCTCT	GACGGCACTT	ATCCGCCTGG	TACTGAGCAA	1980
1981	AACCCCGCTA	ATCCTAATCC	TTCTCTTGAG	GAGTCTCAGC	CTCTTAATAC	TTTCATGTTT	2040
2041	CAGAATAATA	GGTTCCGAAA	TAGGCAGGGG	GCATTAACCTG	TTTATACGGG	CACTGTTACT	2100
2101	CAAGGCACTG	ACCCCGTTAA	AACTTATTAC	CAGTACACTC	CTGTATCATC	AAAAGCCATG	2160
2161	TATGACGCTT	ACTGGAACGG	TAAATTGAGA	GACTGCGGCT	TCCATTCTGG	CTTAAATGAA	2220
2221	GATCCATTTC	TTTGTGAATA	TCAAGGCGAA	TCGTCTGACC	TGCCTCAACC	TCCTGTCAAT	2280
2281	GCTGGCGGGG	GCTCTGGTGG	TGGTTCTGGT	GGCGGCTCTG	AGGGTGGTGG	CTCTGAGGGT	2340
2341	GGCGGTTCTG	AGGGTGGCGG	CTCTGAGGGA	GGCGGTTCCG	GTGDTGGCTC	TGGTTCCGGT	2400
2401	GATTTTGAAT	ATGAAAAGAT	GGCAAAACGCT	AATAAGGGGG	CTATGACCGA	AAATGCCGAT	2460
2461	GAAAACGCGC	TACAGTCTGA	CGCTAAAGGC	AAACTTGATT	CTGTGCTGAC	TGATTACGGT	2520
2521	GCTGCTATCG	ATGGTTTCAAT	TGGTGACGTT	TCCGGCCTTG	CTAATGGTAA	TGGTGCTACT	2580
2581	GGTGATTTTG	CTGGCTCTAA	TTCCCAAATG	GCTCAAGTCG	GTGACGGTGA	TAATTCACCT	2640
2641	TTAATGAATA	ATTTCCGTCA	ATATTTACCT	TCCCTCCCTC	AATCGGTTGA	ATGTCGCCCT	2700
2701	TTTGTCTTTA	GCGCTGGTAA	ACCATATGAA	TTTTCTATTG	ATTGTGACAA	AATAAACTTA	2760
2761	TTCCGTGGTG	TCTTTGCGTT	TCTTTTATAT	GTTGCCACCT	TTATGTATGT	ATTTTCTACG	2820
2821	TTTGCTAACA	TACTGCGTAA	TAAGGAGTCT	TAATCATGCC	AGTTCTTTTG	GGTATTCCGT	2880
2881	TATTATTGCG	TTTCCTCGGT	TTCTTCTGTT	TAACCTTTGT	CGGCTATCTG	CTTAACTTTT	2940
2941	TTAAAAAGGG	CTTCGGTAAG	ATAGCTATTG	CTATTTTCATT	GTTTCTTGCT	CTTATTATTG	3000
3001	GGCTTAACTC	AATTCTTGTG	GGTTATCTCT	CTGATATTAG	CGCTCAATTA	CCCTCTGACT	3060
3061	TTGTTCAAGG	TGTTCAAGTTA	ATTCTCCCGT	CTAATGCGCT	TCCCTGTTTT	TATGTTATTG	3120
3121	TCTCTGTAAA	GGCTGCTATT	TTCATTTTTG	ACGTTAAACA	AAAAATCGTT	TCTTATTTTG	3180
3181	ATTGGGATAA	ATAATATGGC	TGTTTATTTT	GTAAGTGGCA	AATTAGGCTC	TGGAAGACG	3240
3241	CTCGTTAGCG	TTGGTAAGAT	TCAAGGATAA	ATTGTAGCTG	GGTGCAAAAT	AGCAACTAAT	3300
3301	CTTGATTTAA	GGCTTCAAAA	CTCCCGCAAA	GTCGGGAGGT	TCGCTAAAAC	GCCTCGCGTT	3360
3361	CTTAGAATAC	CGGATAAGCC	TTCTATATCT	GATTTGCTTG	CTATTGGGCG	CGGTAATGAT	3420
3421	TCCTACGATG	AAAATAAAAA	CGGCTTGCTT	GTTCTCGATG	AGTGCGGTAC	TTGGTTTAA	3480
3481	ACCCGTTCTT	GGAATGATAA	GGAAAGACAG	CCGATTATTG	ATTGGTTTCT	ACATGCTCGT	3540
3541	AAATTAGGAT	GGGATATTAT	CTTCCTTGTT	CAGGACTTAT	CTATTGTTGA	TAAACAGGCG	3600
3601	CGTTCTGCAT	TAGCTGAACA	TGTTGTTTAT	TGTCGTCGTC	TGGACAGAAT	TACTTTACCT	3660
3661	TTTGTCTGTA	CTTTATATTG	TCTTATTACT	GGCTCGAAAA	TGCCTCTGCC	TAAATTACAT	3720
3721	GTTGGCGTTG	TAAATATGGG	CGATTCTCAA	TTAAGCCCTA	CTGTTGAGCG	TTGGCTTTAT	3780
3781	ACTGGTAAGA	ATTTGTATAA	CGCATATGAT	ACTAAACAGG	CTTTTTCTAG	TAATTATGAT	3840

FIG. 9-1

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3841	TCCGGTGT	TTTCTTAT	AACGCCTT	TTATCACAC	GTCGGTATT	CAAACCAT	3900
3901	AATTTAGG	AGAAGATG	GCTTACTA	ATATATTT	AAAAAGTT	ACGCGTTC	3960
3961	TGCTTTGC	TTGGATTT	ATCAGCAT	ACATATAG	ATATAACCC	ACCTAAGCC	4020
4021	GAGGTTAAA	AGGTAGTCT	TCAGACCT	GATTTTGAT	AATTCACAT	TGACTCTTC	4080
4081	CAGCGTCTT	ATCTAAGCT	TCGCTATG	TTCAAGGAT	CTAAGGGAA	ATTAATTA	4140
4141	AGCGACGAT	TACAGAAGC	AGGTTATT	CTCACATAT	TTGATTTAT	TACTGTTTC	4200
4201	ATTA AAAAG	TAATTCAA	GAAATTGT	AATGTAAT	ATTTTGTTT	CTTGATGTT	4260
4261	GTTTCATCA	CTTCTTTG	TCAGGTA	GAAATGA	ATTCGCCT	GC GCGAT	4320
4321	GTAAC TTGG	ATTC AAAG	ATCAGGCG	TCCGTTATT	TTTCTCCCG	TGTA AAAAG	4380
4381	ACTGTTACT	TATATTCAT	TGACGTTAA	CCTGAAATC	TACGCAAT	CTTTATTT	4440
4441	GTTTTACGT	CTAATAAT	TGATATGG	CCTTCAAT	CTTCCATT	TTAGAAGT	4500
4501	AATCCAAAC	ATCAGGAT	TATTGATG	TTGCCATCA	CTGATAAT	GGAATATG	4560
4561	GATAATTCC	CTCCTTCT	TGGTTTCT	GTTCCGCAA	ATGATAAT	TACTCAAAC	4620
4621	TTTAAATTA	ATAACGTT	GGCAAAGG	TTAATACG	TTGTCGA	GTTTGTAAG	4680
4681	CTAATCTCT	CTAAATCCT	AAATGTATT	TCTATTGAC	GCTCTAAT	ATTAGTTGT	4740
4741	AGTGACCTA	AAGATATTT	AGATAACCT	CCTCAATTC	TTTCTACT	TGATTTGCC	4800
4801	ACTGACCAG	TATTGATTG	GGGTTTGAT	TTTGAGGTT	AGCAAGGT	TGCTTTAG	4860
4861	TTTTCATTT	CTGCTGGCT	TCAGCGTGG	ACTGTTGCA	GCGGTGTTA	TACTGACCG	4920
4921	CTCACCTCT	TTTTATCTT	TGCTGGTGG	TCGTTCCGT	TTTTTAATG	CGATGTTTT	4980
4981	GGGCTATCA	TTGCGGCAT	AAAGACTAA	AGCCATTCA	AAATATTGT	TGTGCCACG	5040
5041	ATTCTTACG	TTTCAGGTCA	GAAGGGTCT	ATCTCTGTT	GCCAGAATG	CCCTTTTAT	5100
5101	ACTGGTCTG	TGACTGGTG	ATCTGCCAT	GTAAATAAT	CATTTCAG	GATTTAGCG	5160
5161	CAAATGTAG	GTATTTCCAT	GAGCGTTTT	CCTGTTGCA	TGGCTGGCG	TAATATTGT	5220
5221	CTGGATATTA	CCAGCAAGG	CGATAGTTT	AGTTCCTCT	CTCAGGCA	TGATGTTAT	5280
5281	ACTAATCAA	GAAGTATTG	TACAACGGT	AATTTGCGT	ATGGACAG	TCTTTTACT	5340
5341	GGTGGCCTC	CTGATTATA	AAACACTCT	CAAGATTCT	GCGTACCGT	CCTGTCTAA	5400
5401	ATCCCTTTA	TCGGCCTCT	GTTTAGCTC	CGCTCTGAT	CCAACGAG	AGAGCTTTA	5460
5461	TACGTGCTG	TCAAAGCA	CATAGTACG	GGCCTGTAG	GGCGCATTA	GCGCGGCGG	5520
5521	TGTGGTGGT	ACGCGCAGC	TGACCGCTA	ACTTGCCAG	GCCCTAGCG	CCGCTCCTT	5580
5581	CGCTTTCTT	CCTTCCTTT	TCGCCACGT	CGCCGGCTT	CCCCGTCA	CTCTAAATC	5640
5641	GGGGCTCCCT	TTAGGGTTCC	GATTTAGTG	TTTACGGCA	CTCGACCCCA	AAAAACTTG	5700
5701	TTTGGGTGAT	GGTTACGTA	TGGGGCCAT	GCCCTGATG	ACGTTTTTTC	GCCCTTTGAC	5760
5761	GTTGGAGTCC	ACGTTCTTTA	ATAGTGGAT	CTTGTTCCAA	ACTGGAACAA	CACCTCAACC	5820
5821	TATCTCGGGC	TATTCTTTTG	ATTTATAAG	GATTTTGCCG	ATTTCGGAAC	CACCATCAA	5880
5881	CAGGATTTTC	GCCTGCTGGG	GCAAACCAG	GTGGACCGCT	TGCTGCAACT	CTCTCAGGG	5940
5941	CAGGCGGTGA	AGGGCAATCA	GCTGTTGCC	GTCTCGCTGG	TGAAAAGAAA	AACCACCCTG	6000
6001	GCGCCCAATA	CGCAAACCG	CTCTCCCCG	GCGTTGGCCG	ATTCATTAAT	GCAGCTGGCA	6060
6061	CGACAGGTTT	CCCGACTGGA	AAGCGGGCAG	TGAGCGCAAC	GCAATTAATG	TGAGTTAGCT	6120
6121	CACCTATTAG	GCACCCAGG	CTTTACACTT	TATGCTTCCG	GCTCGTATGT	TGTGTGGAAT	6180
6181	TGTGAGCGGA	TAACAATTT	ACACAGGAAA	CAGCTATGAC	CAGGATGTAC	GAATTCGCAG	6240
6241	GTAGGAGAGC	TCGGCGGATC	CGAGGCTGAA	GGCGATGACC	CTGCTAAGGC	TGCATTCAAT	6300
6301	AGTTTACAGG	CAAGTGCTAC	TGAGTACATT	GGCTACGCTT	GGGCTATGGT	AGTAGTTATA	6360
6361	GTTGGTGCTA	CCATAGGGAT	TAAATTATTC	AAAAAGTTTA	CGAGCAAGGC	TTCTTAACCA	6420
6421	GCTGGCGTAA	TAGCGAAGAG	GCCCGCACCG	ATCGCCCTTC	CCAACAGTTG	CGCAGCCTGA	6480
6481	ATGGCGAATG	GCGCTTTGCC	TGGTTTCCGG	CACCAGAAGC	GGTGCCGGAA	AGCTGGCTGG	6540
6541	AGTGCGATCT	TCCTGAGGCC	GATACGGTCG	TCGTCCCCTC	AAACTGGCAG	ATGCACGGTT	6600
6601	ACGATGCGCC	CATCTACACC	AACGTAACCT	ATCCCATTA	GGTCAATCCG	CCGTTTGTT	6660
6661	CCACGGAGAA	TCCGACGGGT	TGTTACTCGC	TCACATTTAA	TGTTGATGAA	AGCTGGCTAC	6720
6721	AGGAAGGCCA	GACGCGAATT	ATTTTTGATG	CGCTTCTAT	TGGTTAAAAA	ATGAGCTGAT	6780
6781	TTAACAAAAA	TTTAACGCGA	ATTTTAAACA	AATATTAACG	TTTACAATTT	AAATATTTGC	6840
6841	TTATACAATC	TTCTGTGTTT	TGGGGCTTTT	CTGATTATCA	ACCGGGGTAC	ATATGATTGA	6900
6901	CATGCTAGTT	TTACGATTAC	CGTTCATCGA	TTCTCTTGTT	TGCTCCAGAC	TCTCAGGCAA	6960
6961	TGACCTGATA	GCCTTTGTAG	ATCTCTCAAA	AATAGCTACC	CTCTCCGGCA	TTAATTTATC	7020
7021	AGCTAGAACG	GTTGAATATC	ATATTGATGG	TGATTGACT	GTCTCCGGCC	TTTCTCACC	7080
7081	TTTTGAATCT	TTACCTACAC	ATTACTCAGG	CATTGCATTT	AAAAATATG	AGGGTTCTAA	7140
7141	AAATTTTAT	CCTTGCGTTG	AAATAAAGG	TTCTCCCGCA	AAAGTATTAC	AGGGTCATAA	7200
7201	TGTTTTTGGT	ACAACCGATT	TAGCTTTATG	CTCTGAGGCT	TTATTGCTTA	ATTTTGCTAA	7260
7261	TTCTTTGCCT	TGCCTGTATG	ATTTATTGGA	CGTT			7294

FIG. 9-2

	10	20	30	40	50	60	
1	AATGCTACTA	CTATTAGTAG	AATTGATGCC	ACCTTTTCAG	CTCGCGCCCC	AAATGAAAAT	60
61	ATAGCTAAAC	AGGTTATTGA	CCATTTGCGA	AATGTATCTA	ATGGTCAAAC	TAAATCTACT	120
121	CGTTTCGAGA	ATTGGGAATC	AACTGTTACA	TGGAATGAAA	CTTCCAGACA	CCGTACTTTA	180
181	GTTGCATATT	TAAAACATGT	TGAGCTACAG	CACCAGATTC	AGCAATTAAG	CTCTAAGCCA	240
241	TCTGCAAAAA	TGACCTCTTA	TCAAAAGGAG	CAATTAAGG	TACTCTCTAA	TCCTGACCTG	300
301	TTGGAGTTTG	CTTCCGGTCT	GGTTTCGCTT	GAAGCTCGAA	TTAAAACGCG	ATATTTGAAG	360
361	TCTTTCCGGC	TTCTCTTAA	TCTTTTGTAT	GCAATCCGCT	TTCGTTCTGA	CTATAATAGT	420
421	CAGGGTAAAG	ACCTGATTTT	TGATTTATGG	TCATTCTCGT	TTTCTGAAGT	GTTTAAAGCA	480
481	TTTGAGGGGG	ATTCAATGAA	TATTTATGAC	GATTCCGCAG	TATTGGACGC	TATCCAGTCT	540
541	AAACATTTTA	CTATTACCCC	CTCTGGCAAA	ACTTCTTTTG	CAAAAGCCTC	TCGCTATTTT	600
601	GGTTTTTATC	GTCGTCTGGT	AAACGAGGGT	TATGATAGTG	TTGCTCTTAC	TATGCCTCGT	660
661	AATTCCTTTT	GGCGTTATGT	ATCTGCATTA	GTTGAATGTG	GTATTCCTAA	ATCTCAACTG	720
721	ATGAATCTTT	CTACCTGTAA	TAATGTTGTT	CCGTTACTTC	GTTTTATTAA	CGTAGATTTT	780
781	TCTTCCCAAC	GTCCTGACTG	GTATAATGAG	CCAGTTCTTA	AAATCGCATA	AGGTAATTCA	840
841	CAATGATTAA	AGTTGAAATT	AAACCATCTC	AAGCCCAATT	TACTACTCGT	TCTGGTGTTC	900
901	CTCGTCAGGG	CAAGCCTTAT	TCACTGAATG	AGCAGCTTTG	TTACGTTGAT	TTGGGTAATG	960
961	AATATCCGGT	TCTTGTCAGG	ATTACTCTTG	ATGAAGGTCA	GCCAGCCTAT	GCGCCTGGTC	1020
1021	TGTACACCGT	TCATCTGTCC	TCTTTCAGAG	TTGGTCAGTT	CGGTTCCCTT	ATGATTGACC	1080
1081	GTCTGCGCCT	CGTTCCGGCT	AAGTAACATG	GAGCAGGTGC	CGGATTTCTG	CACAATTTAT	1140
1141	CAGGCGATGA	TACAAATCTC	CGTTGTACTT	TGTTTCGCGC	TTGGTATAAT	CGCTGGGGGT	1200
1201	CAAAGATGAG	TGTTTTAGTG	TATTTCTTCG	CCTCTTTCGT	TTTAGGTTGG	TGCCTTCGTA	1260
1261	GTGGCATTAC	GTATTTTACC	CGTTTAATGG	AAACTTCCTC	ATGAAAAAGT	CTTTAGTCCT	1320
1321	CAAAGCCTCT	GTAGCCGTTG	CTACCCTCGT	TCCGATGCTG	TCTTTCGCTG	CTGAGGGTGA	1380
1381	CGATCCCGCA	AAAGCGGCCT	TTAACTCCCT	GCAAGCCTCA	GCGACCGAAT	ATATCGGTTA	1440
1441	TGCGTGGGCG	ATGGTTGTTG	TCATTGTGCG	CGCAACTATC	GGTATCAAGC	TGTTTAAAGAA	1500
1501	ATTCACCTCG	AAAGCAAGCT	GATAAACCAG	TACAATTAAG	GGCTCCTTTT	GGAGCCTTTT	1560
1561	TTTTTGAGAG	TTTTCAACGT	GAAAAAATTA	TTATTCGCAA	TTCTTTTAGT	TGTTCCCTTC	1620
1621	TATTTCTACT	CCGCTGAAAC	TGTTGAAAGT	TGTTTAGCAA	AACCCCATAC	AGAAAAATTCA	1680
1681	TTTACTAACG	TCTGGAAAGA	GCACAAAAC	TTAGATCGTT	ACGCTAACTA	TGAGGGTTGT	1740
1741	CTGTGGAATG	CTACAGGCGT	TGTAGTTTGT	ACTGGTGACG	AAACTCAGTG	TTACGGTACA	1800
1801	TGGGTTCTTA	TTGGGCTTGC	TATCCCTGAA	AATGAGGGTG	GGTGCTCTGA	GGTGCGCGGT	1860
1861	TCTGAGGGTG	GCGGTTCTGA	GGGTGGCGGT	ACTAAACCTC	CTGAGTACGG	TGATACACCT	1920
1921	ATTCGGGGCT	ATACTTATAT	CAACCCTCTC	GACGGCACTT	ATCCGCCTGG	TACTGAGCAA	1980
1981	AACCCCGCTA	ATCCTAATCC	TTCTCTTGAG	GAGTCTCAGC	CTCTTAATAC	TTTCATGTTT	2040
2041	CAGAATAATA	GGTTCCGAAA	TAGGCAGGGG	GCATTAAGTG	TTTATACGGG	CACTGTTACT	2100
2101	CAAGGCATCG	ACCCCGTTAA	AACTTATTAC	CAGTACATCT	CTGTATCATC	AAAAGCCATG	2160
2161	TATGACGCTT	ACTGGAACGG	TAAATTCAGA	GACTGCGCTT	TCCATTCTGG	CTTTAATGAA	2220
2221	GATCCATTCTG	TTTGTGAATA	TCAAGGCCAA	TCGTCTGACC	TGCCTCAACC	TCCTGTCAAT	2280
2281	GCTGGCGGCG	GCTCTGGTGG	TGGTCTGGT	GGCGGCTCTG	AGGGTGGTGG	CTCTGAGGGT	2340
2341	GGCGGTTCTG	AGGGTGGCGG	CTCTGAGGGA	GGCGGTTCCG	GTGGTGGCTC	TGGTTCGGGT	2400
2401	GATTTTGATT	ATGAAAAGAT	GGCAACGCT	AATAAGGGGG	CTATGACCGA	AAATGCCGAT	2460
2461	GAAAAACGCG	TACAGTCTGA	CGCTAAAGGC	AAACTTGATT	CTGTGCTGAC	TGATTACGGT	2520
2521	GCTGCTATCG	ATGGTTTCAT	TGGTGACGTT	TCCGGCCTTG	CTAATGGTAA	TGGTGCTACT	2580
2581	GGTGATTTTG	CTGGCTCTAA	TTCCCAAATG	GCTCAAGTCG	GTGACGGTGA	TAATTCACCT	2640
2641	TTAATGAATA	ATTTCCGTCA	ATATTTACCT	TCCCTCCCTC	AATCGGTTGA	ATGTCGCCCT	2700
2701	TTTGTCTTTA	GCGCTGGTAA	ACCATATGAA	TTTTCTATTG	ATTGTGACAA	AATAAACTTA	2760
2761	TTCCGTGGTG	TCTTTGCGTT	TCTTTTATAT	GTTGCCACCT	TTATGTATGT	ATTTTCTACG	2820
2821	TTTGCTAACA	TACTGCGTAA	TAAGGAGTCT	TAATCATGCC	AGTTCTTTTG	GGTATTCCGT	2880
2881	TATTATTGCG	TTTCCTCGGT	TTCTTCTGTT	TAACCTTGTG	CGGCTATCTG	CTTACTTTTC	2940
2941	TTAAAAAGGG	CTTCGGTAAG	ATAGCTATTG	CTATTTTCAT	GTTTCTTGCT	CTTATTATTG	3000
3001	GGCTTAACTC	AATTCCTGTG	GGTTATCTCT	CTGATATTAG	CGCTCAATTA	CCCTCTGACT	3060
3061	TTGTTACAGG	TGTTTCAGTTA	ATTCTCCCGT	CTAATGCGCT	TCCCTGTTTT	TATGTTATTC	3120
3121	TCTCTGTAAA	GGCTGCTATT	TTCAATTTTG	ACGTTAAACA	AAAAATCGTT	TCTTATTTGG	3180
3181	ATTGGGATAA	ATAATATGGC	TGTTTATTTT	GTAATGGGCA	AATTAGGCTC	TGGAAGACG	3240
3241	CTCGTTAGCG	TTGGTAAGAT	TTAGGATAAA	ATTGTAGCTG	GGTGCAAAAT	AGCAACTAAT	3300
3301	CTTGATTTAA	GGCTTCAAAA	CCTCCCGCAA	GTCGGGAGGT	TCGCTAAAAC	GCCTCGCGTT	3360
3361	CTTAGAATAC	CGGATAAGCC	TTCTATATCT	GATTTGCTTG	CTATTGGGCG	CGGTAATGAT	3420
3421	TCCTACGATG	AAAATAAAAA	CGGCTTGCTT	GTTCTCGATG	AGTGCGGTAC	TTGGTTTAA	3480
3481	ACCCGTTCTT	GGAAATGATA	GGAAAGACAG	CCGATTATTG	ATTGGTTTCT	ACATGCTCGT	3540
3541	AAATTAGGAT	GGGATATTAT	TTTTCTTGTT	CAGGACTTAT	CTATTGTTGA	TAAACAGGCG	3600
3601	CGTTCTGCAT	TAGCTGAACA	TGTTGTTTAT	TGTCGTCGTC	TGGACAGAAT	TACTTTACCT	3660
3661	TTTGTGCGTA	CTTTATATTG	TCTTATTACT	GGCTCGAAAA	TGCCTCTGCC	TAAATTACAT	3720
3721	GTTGGCGTTG	TTAAATATGG	CGATTCTCAA	TTAAGCCCTA	CTGTTGAGCG	TTGGCTTTAT	3780
3781	ACTGGTAAGA	ATTTGTATAA	CGCATATGAT	ACTAAACAGG	CTTTTTCTAG	TAATTATGAT	3840

FIG. 10-1

SUBSTITUTE SHEET

3841	TCCGGTGTTT	ATTCTTATTT	AACGCCTTAT	TTATCACACG	GTCGGTATTT	CAAACCATTA	3900
3901	AATTTAGGTC	AGAAGATGAA	GCTTACTAAA	ATATATTTGA	AAAAGTTTTT	ACGCGTTCTT	3960
3961	TGTCTTGCGA	TTGGATTTGC	ATCAGCATTT	ACATATAGTT	ATATAACCCA	ACCTAAGCCG	4020
4021	GAGGTTAAAA	AGGTAGTCTC	TCAGACCTAT	GATTTTGATA	AATTCACAT	TGACTCTTCT	4080
4081	CAGCGTCTTA	ATCTAAGCTA	TCGCTATGTT	TTCAAGGATT	CTAAGGGAAA	ATTAATTAAT	4140
4141	AGCGACGATT	TACAGAAGCA	AGGTTATTCA	CTCACATATA	TTGATTTATG	TACTGTTTCC	4200
4201	ATTAATAAAG	GTAATTCAAA	TGAAATTGTT	AAATGTAATT	AATTTTGTTT	TCTTGATGTT	4260
4261	TGTTTCATCA	TCTTCTTTTG	CTCAGGTAAT	TGAAATGAAT	AATTCGCCTC	TGCGCGATTT	4320
4321	TGTAACCTTG	TATTCAAAGC	AATCAGGCGA	ATCCGTTATT	GTTTCTCCCG	ATGTAAAAGG	4380
4381	TACTGTTACT	GTATATTAT	CTGACGTTAA	ACCTGAAAAT	CTACGCAATT	TCTTTATTTT	4440
4441	TGTTTACAGT	GCTAATAATT	TTGATATGGT	TGGTTCAATT	CCTTCCATAA	TTCAGAAGTA	4500
4501	TAATCCAAAC	AATCAGGATT	ATATTGATGA	ATTGCCATCA	TCTGATAAT	AGGAATATGA	4560
4561	TGATAATTCC	GCTCCTTCTG	GTGGTTTCTT	TGTTCCGCAA	AATGATAATG	TTACTCAAAC	4620
4621	TTTTAAATTT	AATAACGTTT	GGGCAAAGGA	TTTAATACGA	GTTGTGCAAT	TGTTTGTAAT	4680
4681	GTCTAATACT	TCTAAATCCT	CAAATGTATT	ATCTATTGAC	GGCTCTAATC	TATTAGTTGT	4740
4741	TAGTGCACCT	AAAGATATTT	TAGATAACCT	TCTCAATTTC	CTTCTACTTG	TTGATTTGCC	4800
4801	AAC TGACCA	ATATTGATTG	AGGGTTTGTG	ATTTGAGGTT	CAGCAAGGTT	ATGCTTTAGA	4860
4861	TTTTTTCATT	GCTGCTGGCT	CTCAGCGTGG	CACCTGTTGCA	GGCGGTGTTA	ATACTGACCG	4920
4921	CCTCACCTCT	GTTTTATCTT	CTGCTGGTGG	TCTGTTGCGT	ATTTTAAATG	CGCATGTTTT	4980
4981	AGGGCTATCA	GTTTCGCGCAT	TAAAGACTAA	TAGCCATTCA	AAAATATTGT	CTGTGCCACG	5040
5041	TATTTCTTACG	CTTTCAGGTC	AGAAGGGTTC	TATCTCTGTT	GGCCAGAATG	TCCCTTTTAT	5100
5101	TACTGGTCGT	GTGACTGGTG	AATCTGCCAA	TGTAAATAAT	CCATTTTCAGA	CGATTGAGCG	5160
5161	TCAAAATGTA	GGTATTTCCA	TGAGCGTTTT	TCCTGTTGCA	ATGGCTGGCG	GTAATATTGT	5220
5221	TCTGGATATT	ACCAGCAAGG	CCGATAGTTT	GAGTTCTTCT	ACTCAGGCAA	GTGATGTTAT	5280
5281	TACTAATCAA	AGAAGTATTG	CTACAACGGT	TAATTTGCGT	GATGGACAGA	CTCTTTTACT	5340
5341	CGGTGGCCTC	ACTGATTATA	AAAACACTTC	TCAAGATTCT	GGCGTACCGT	TCCTGTCTAA	5400
5401	AATCCCTTTA	ATCGGCCCTC	TGTTTAGCTC	CCGCTCTGAT	TCCAACGAGG	AAAGCACGTT	5460
5461	ATACGTGCTC	GTCAAAGCAA	CCATAGTAGC	CGCCCTGTAG	CGGCGCATTA	AGCGCGGCGG	5520
5521	GTGTGGTGGT	TACGCGCAGC	GTGACCGCTA	CACCTTGCCAG	CGCCCTAGCG	CCCGCTCCTT	5580
5581	TCGCTTTCTT	CCCTTCTTTT	CTCGCCACGT	TCGCGGCTTT	TCCCGTCAA	GCTCTAAATC	5640
5641	GGGGGCTCCC	TTTAGGGTTC	CGATTTAGTG	CTTTACGGCA	CCTCGACCCC	AAAAAACTTG	5700
5701	ATTTGGGTGA	TGGTTCACGT	AGTGGGCCAT	CGCCCTGATA	GACGGTTTTT	CGCCCTTTGA	5760
5761	CGTTGGAGTC	CACGTTCTTT	AATAGTGGAC	TCTTGTTCCA	AACTGGAACA	AACTCAACC	5820
5821	CTATCTCGGG	CTATTCTTTT	GATTTATAAG	GGATTTTGCC	GATTTGCGAA	CCACCATCAA	5880
5881	ACAGGATTTT	CGCCTGCTGG	GGCAAACGAG	CGTGGACCGC	TTGCTGCAAC	TCTCTCAGGG	5940
5941	CCAGGCGGTG	AAGGGCAATC	AGCTGTTGCC	CGTCTCGCTG	GTGAAAAGAA	AAACCACCTT	6000
6001	GGCGCCCAAT	ACGCAAACCG	CCTCTCCCGG	CGCGTTGGCC	GATTCATTAA	TGCAGCTGGC	6060
6061	ACGACAGGTT	TCCCGACTGG	AAAGCGGGCA	GTGAGCGCAA	CGCAATTAAT	GTGAGTTAGC	6120
6121	TCACTCATTA	GGCACCCAG	GCTTTACACT	TTATGCTTCC	GGCTCGTATG	TTGTGTGGAA	6180
6181	TTGTGAGCGG	ATAACAATTT	CACACGCGTC	ACTTGGCACT	GGCCGTCGTT	TTACAACGTC	6240
6241	GTGACTGGGA	AAACCCTGGC	GTTACCCAAG	CTTTGTACAT	GGAGAAAATA	AAGTGAAACA	6300
6301	AAGCACTATT	GCACTGGCAC	TCTTACCGTT	ACTGTTTACC	CCTGTGGCAA	AAGCCCTTCT	6360
6361	GAGGCATCCG	GGAGCTGAAG	GCGATGACCC	TGCTAAGGCT	GCATTCAATA	GTTTACAGGC	6420
6421	AAGTGCTACT	GAGTACATTG	GCTACGCTTG	GGCTATGGTA	GTAGTTATAG	TTGGTGCTAC	6480
6481	CATAGGGATT	AAATTATTCA	AAAAGTTTAC	GAGCAAGGCT	TCTTAAGCAA	TAGCGAAGAG	6540
6541	GCCCGCACCG	ATCGCCCTTC	CCAACAGTTG	CGCAGCCTGA	ATGGCGAATG	GCGCTTTGCC	6600
6601	TGGTTTCCGG	CACCAGAAGC	GGTGCCGGAA	AGCTGGCTGG	AGTGCATCT	TCCTGAGGCC	6660
6661	GATACGGTCG	TCGTCCCCTC	AAACTGGCAG	ATGCACGGTT	ACGATGCGCC	CATCTACACC	6720
6721	AACGTAACCT	ATCCCATTAC	GGTCAATCCG	CCGTTTGTTT	CCACGGAGAA	TCCGACGGGT	6780
6781	TGTTACTCGC	TCACATTTAA	TGTTGATGAA	AGCTGGCTAC	AGGAAGGCCA	GACGCGAATT	6840
6841	ATTTTIGATG	GCGTTCCTAT	TGGTTAAAAA	ATGAGCTGAT	TTAACAAAAA	TTTAACGCGA	6900
6901	AATTTAAACA	AATATTAACG	TTTACAATTT	AAATATTTGC	TTATACAATC	TTCTGTGTTT	6960
6961	TGGGGCTTTT	CTGATTATCA	ACCGGGGTAC	ATATGATTGA	CATGCTAGTT	TTACGATTAC	7020
7021	CGTTCATCGA	TTCTCTTGTT	TGCTCCAGAC	TCTCAGGCAA	TGACCTGATA	TTCTTTGTAG	7080
7081	ATCTCTCAAA	AATAGCTACC	CTCTCCGGCA	TTAATTTATC	AGCTAGAACG	GTTGAATATC	7140
7141	ATATTGATGG	TGATTTGACT	GTCTCCGGCC	TTTCTCACCC	TTTTGAATCT	TTACCTACAC	7200
7201	ATTACTCAGG	CATTGCATTT	AAAATATATG	AGGGTTCTAA	AAATTTTTAT	CCTTGCGTTG	7260
7261	AAATAAAGGC	TTCTCCCGCA	AAAGTATTAC	AGGGTCATAA	TGTTTTTGGT	ACAACCGATT	7320
7321	TAGCTTTATG	CTCTGAGGCT	TTATTGCTTA	ATTTTGCTAA	TTCTTTGCCT	TGCCTGTATG	7380
7381	ATTTATTGGA	CGTT					7394

FIG. 10-2

SUBSTITUTE SHEET

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US93/10850

A. CLASSIFICATION OF SUBJECT MATTER

IPC(5) : C12N 15/00, 15/11, 15/62, 15/67, 15/70; C07H 21/04; C08G 69/02

US CL : Please See Extra Sheet.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : Please See Extra Sheet.

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y,P	US, A, 5,185,147 (Papsidero) 09 February 1993, col. 2, 7, 8, 10.	1-46
Y	The Journal of Biological Chemistry, Volume 266, No. 33, issued 25 November 1991, B. M. Olivera et al, "Conotoxins", pages 22067-22070, see entire document.	1-46
Y	Proceedings of the National Academy of Science USA, Volume 87, issued August 1990, S. E. Cwirla et al, "Peptides on Phage: A Vast Library of Peptides for Identifying Ligands", pages 6378-6382, see entire document.	1-46

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	*T	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be part of particular relevance	*X*	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	*Y*	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*Z*	document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means		
P document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

04 FEBRUARY 1994

Date of mailing of the international search report

APR 06 1994

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

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Form PCT/ISA/210 (second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.

T/US93/10850

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Science, Volume 249, issued 27 July 1990, J. J. Devlin et al, "Random Peptide Libraries: a Source of Specific Protein Binding Molecules", pages 404-406, see entire document.	1-46
Y	European Journal of Immunology, Volume 20, issued March 1990, R. Jemmerson et al, "Fine Manipulation of Antibody Affinity for Synthetic Epitopes by Altering Peptide Structure: Antibody Binding to Looped Peptides", pages 579-585, see entire document.	1-46
Y	Gene, Volume 44, issued August 1986, A. R. Oliphant et al, "Cloning of Random-Sequence Oligodeoxynucleotides", pages 177-183, see entire document.	1-46
Y	Gene, Volume 73, issued 20 December 1988, S. F. Parmley et al, Antibody-Selectable Filamentous fd Phage Vectors: Affinity Purification of Target Genes", pages 305-318, see entire document.	7,17,19,20,21,36
Y	Proceedings of the National Academy of Sciences USA, Volume 89, issued May 1992, R. N. Zuckermann et al, "Identification of Highest-Affinity Ligands by Affinity Selection from Equimolar Peptides Mixtures Generated by Robotic Synthesis", pages 4505-4509, see entire document.	1-46
A	Proceedings of the National Academy of Sciences USA, Volume 84, issued December 1987, T. M. Fieser et al, "Influence of Protein Flexibility and Protein Conformation of Reactivity of Monoclonal Anti-Peptide Antibodies with a Protein Alpha Helix", pages 8568-8572, see entire document.	1-46
A	The EMBO Journal, Volume 9, No. 9, issued September 1990, A. Gallusser et al, "Initial Steps of Protein Membrane Insertion. Bacteriophage M13 Procoat Protein Binds to the Membrane Surface by Electrostatic Interaction", pages 2723-2729, see entire document.	7,17,19,20,21,36
A	European Journal of Biochemistry, Volume 177, issued November 1988, A. Kuhn, "Alterations in the Extracellular Domain of M13 Procoat Protein Make its Membrane Insertion Dependent on <u>secA</u> and <u>secY</u> ", pages 267-271, see entire document.	7,17,19,20,21,36

INTERNATIONAL SEARCH REPORTInternational application No.
PCT/US93/10850**C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT**

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	The EMBO Journal, Volume 4, No. 7, issued July 1985, U. Schultz-Gahmen et al, "Towards Assignment of Secondary Structures by Anti-Peptide Antibodies. Specificity of the Immune Response to a Beta Turn", pages 1731-1737, see entire document.	1-46

A. CLASSIFICATION OF SUBJECT MATTER:
US CL :

435/69.1, 69.7, 69.8, 172.3, 235.1, 320.1; 530/300; 536/22.1, 23.4, 23.72, 25.3

B. FIELDS SEARCHED

Minimum documentation searched

Classification System: U.S.

435/69.1, 69.7, 69.8, 172.3, 235.1, 320.1; 530/300; 536/22.1, 23.4, 23.72, 25.3

B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

APS, DIALOG, search terms: M13, geneVIII, gVIII, geneIII gIII, coat protein, secondary structure, conformation, affinity, antibody, synthetic, soluble, random peptide or oligonucleotide, unbiased or nonbiased, nondegenerate, disulfide, covalent bond